

## **Methods and Compositions for Treating Disorders Involving Excitotoxicity**

### ***Related Applications***

The present application is a continuation-in-part of USSN 09/238,243, filed 27 January 1999,  
5 the specification of which is incorporated by reference herein.

### ***Background of the Invention***

The excessive or inappropriate stimulation of excitatory amino acid receptors can lead to neuronal cell damage or loss by way of a mechanism known as excitotoxicity. For  
10 instance, excitotoxic action may be responsible for neuronal loss in stroke, cerebral palsy, epilepsy, ageing and Alzheimer's disease, Huntington's disease, and other chronic degenerative disorders. The medical consequences of such neuronal degeneration makes the abatement of these degenerative neurological processes an important therapeutic goal.

The development of neuroprotective agents for the prevention of neuronal loss in  
15 acute conditions such as stroke and epilepsy or chronic neurodegenerative disorders including Parkinson's disease, Alzheimer's disease, Huntington's chorea, and motor neuron disease has in fact focused on drugs that inhibit excitatory amino acid neurotransmission or exhibit antioxidant properties. Unfortunately, potent antagonists of the N-methyl-D-aspartate (NMDA) type glutamate receptor, which is thought to mediate excitotoxic neuronal injury,  
20 e.g., MK-801 or phencyclidine (PCP), share a high probability of inducing psychotomimetic side effects. Further, these drugs have been associated with acute neurotoxicity in vitro and in vivo, precluding their clinical use.

It is a goal of the present invention to provide compositions and methods for preventing or ameliorating neuronal degeneration, e.g., for the abatement of these  
25 degenerative neurological processes.

### ***Summary of the Invention***

One aspect of the present application relates to a method for promoting survival and/or functional performance of neuronal cells susceptible to exotoxicity, comprising  
30 contacting the cells, *in vitro* or *in vivo*, with a *hedgehog* therapeutic or *ptc* therapeutic in an amount effective increasing the rate of survival of the neurons relative to the absence of administration of the *hedgehog* therapeutic or *ptc* therapeutic. In preferred embodiments,

the method is carried out using a lipophilic modified *hedgehog* polypeptide effective to reduce exotoxin-mediated degradation of the cells.

For instance, the present application provides a method for promoting the survival of dopaminergic or GABAergic neurons by contacting the cells, *in vitro* or *in vivo*, with a *hedgehog* therapeutic or *ptc* therapeutic in an amount effective to increase the rate of survival of the neurons relative to the absence of administration of the *hedgehog* therapeutic or *ptc* therapeutic.

In other embodiments, the present application relates to a method for promoting the survival of neurons of the substantia nigra by contacting the cells, *in vitro* or *in vivo*, with a *hedgehog* therapeutic or *ptc* therapeutic in an amount effective to increase the rate of survival of the neurons relative to the absence of administration of the *hedgehog* therapeutic or *ptc* therapeutic.

In certain embodiments, the subject invention provides a method for treatment or prophylaxis of a disorder selected from the group consisting of

domoic acid poisoning; spinal cord trauma; hypoglycemia; mechanical trauma to the nervous system; senile dementia; Korsakoff's disease; schizophrenia; AIDS dementia, multi-infarct dementia; mood disorders; depression; chemical toxicity; neuronal damage associated with uncontrolled seizures, such as epileptic seizures; neuronal injury associated with HIV and AIDS; neurodegeneration associated with Down's syndrome; neuropathic pain syndrome; olivopontocerebral atrophy; amyotrophic lateral sclerosis; mitochondrial abnormalities; Alzheimer's disease; hepatic encephalopathy; Tourette's syndrome; schizophrenia; and drug addiction,

comprising administering to a patient in need thereof a therapeutically effective amount of a *hedgehog* or *ptc* therapeutic, e.g., a lipophilic modified *hedgehog* polypeptide.

In other embodiments, the subject method can be used for protecting dopaminergic and/or GABAergic neurons of a mammal from neurodegeneration; for preventing or treating neurodegenerative disorder; for treatment of Parkinson's; for treatment of Huntington's; and/or for treatment of ALS. In embodiments wherein the patient is treated with a *ptc* therapeutic, such therapeutics are preferably small organic molecules which mimic *hedgehog* effects on *patched*-mediated signals.

When the subject method is carried out using a *hedgehog* therapeutic, the *hedgehog* therapeutic preferably is a polypeptide including at least a bioactive extracellular portion of a *hedgehog* polypeptide, e.g., including at least 50, 100 or 150 amino acid residues of an N-terminal half of a *hedgehog* polypeptide. In preferred embodiments, the *hedgehog* portion

includes at least a portion of the *hedgehog* polypeptide corresponding to a 19kd fragment of the extracellular domain of a *hedgehog* polypeptide.

5 In preferred embodiments, the *hedgehog* portion has an amino acid sequence at least 60, 75, 85, 95 or 100 percent identical with a *hedgehog* polypeptide of any of SEQ ID Nos. 10-18 or 20. The *hedgehog* portion can be encoded by a nucleic acid which hybridizes under stringent conditions to a nucleic acid sequence of any of SEQ ID Nos. 1-9 or 19, e.g., the *hedgehog* portion can be encoded by a vertebrate *hedgehog* gene, especially a human *hedgehog* gene.

10 In certain embodiments, the *hedgehog* polypeptides of the present invention are modified by a lipophilic moiety or moieties at one or more internal sites of the mature, processed extracellular domain, and may or may not be also derivatized with lipophilic moieties at the N or C-terminal residues of the mature polypeptide. In other embodiments, the polypeptide is modified at the C-terminal residue with a hydrophobic moiety. In still other embodiments, the polypeptide is modified at the N-terminal residue with a cyclic  
15 (preferably polycyclic) lipophilic group. Various combinations of the above are also contemplated.

In other embodiments, the subject method can be carried out by administering a gene activation construct, wherein the gene activation construct is deigned to recombine with a genomic *hedgehog* gene of the patient to provide a heterologous transcriptional regulatory  
20 sequence operatively linked to a coding sequence of the *hedgehog* gene.

In still other embodiments, the subject method can be practiced with the administration of a gene therapy construct encoding a *hedgehog* polypeptide. For instance, the gene therapy construct can be provided in a composition selected from a group consisting of a recombinant viral particle, a liposome, and a poly-cationic nucleic acid binding agent,

25 In certain embodiments, the polypeptide is purified to at least 80% by dry weight, and more preferably 90 or 95% by dry weight.

Another aspect of the present invention provides an isolated nucleic acid encoding a polypeptide comprising a *hedgehog* amino acid sequence which (i) binds to a *patched* protein, (ii) regulates differentiation of neuronal cells, (iii) regulates survival of differentiated  
30 neuronal cells, (iv) regulates proliferation of chondrocytes, (v) regulates proliferation of testicular germ line cells, or (vi) functionally replaces *drosophila hedgehog* in transgenic *drosophila* fly, or a combination thereof.

In other preferred embodiments, the isolated nucleic acid encodes a polypeptide having a *hedgehog* amino acid sequence encoded by a nucleic acid which hybridizes under  
35 stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID No:1-9, which *hedgehog* amino acid sequence of the polypeptide corresponds to a natural

proteolytic product of a *hedgehog* polypeptide. Such polypeptides preferably (i) binds to a *patched* protein, (ii) regulates differentiation of neuronal cells, (iii) regulates survival of differentiated neuronal cells, (iv) regulates proliferation of chondrocytes, (v) regulates proliferation of testicular germ line cells, and/or (vi) functionally replaces *drosophila* *hedgehog* in transgenic *drosophila* fly, or a combination thereof.

In preferred embodiments, the nucleic acid encodes a *hedgehog* amino acid sequence identical to a *hedgehog* polypeptide selected from the group consisting of SEQ ID No: 10-18.

Another preferred embodiment provides an isolated nucleic acid comprising a coding sequence of a human *hedgehog* gene, encoding a bioactive *hedgehog* polypeptide.

10 Still another aspect of the present invention relates to an expression vector, capable of replicating in at least one of a prokaryotic cell and eukaryotic cell, comprising a nucleic acid encoding a *Dhh* or *Ihh* polypeptide described above.

The present invention also provides a host cell transfected with such expression vectors; as well as methods for producing a recombinant *hedgehog* polypeptide by culturing  
15 such cells in a cell culture medium to express a *hedgehog* polypeptide and isolating said *hedgehog* polypeptide from the cell culture.

Still another aspect of the present invention provides a recombinant transfection system, e.g., such as may be useful for gene therapy, comprising (i) a gene construct including the coding sequence for a human *Ihh* or *Dhh* protein, operably linked to a  
20 transcriptional regulatory sequence for causing expression of the *hedgehog* polypeptide in eukaryotic cells, and (ii) a gene delivery composition for delivering said gene construct to a cell and causing the cell to be transfected with said gene construct. For instance, the gene delivery composition is selected from a group consisting of a recombinant viral particle, a liposome, and a poly-cationic nucleic acid binding agent.

25 Another aspect of the present invention provides a probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of SEQ ID No. 1-9, or naturally occurring mutants thereof. In preferred embodiments, the probe/primer includes a label group attached thereto and able to  
30 be detected. The present invention also provides a test kit for detecting cells which contain a *hedgehog* mRNA transcript, and includes such probe/primers.

Still another embodiment of the present invention provides a purified preparation of an antisense nucleic acid which specifically hybridizes to and inhibits expression of a gene encoding a human *Shh*, *Ihh* or *Dhh* *hedgehog* polypeptide under physiological conditions,  
35 which nucleic acid is at least one of (i) a synthetic oligonucleotide, (ii) single-stranded, (iii)



linear, (iv) 20 to 50 nucleotides in length, and (v) a DNA analog resistant to nuclease degradation.

### Brief Description of the Drawings

Figure 1. *Shh* and *Ptc* in the E14.5 rat embryo. *Shh* (A, antisense; B, sense control), and *ptc* (C, antisense; D, sense control) expression as detected by in situ hybridization with digoxigenin-labeled riboprobes and alkaline phosphataseconjugated anti-digoxigenin. The arrow in A and the double-arrow in C designate the zona limitan intrathalamica. Major anatomical structures and summary diagrams of *shh* and *ptc* expression are shown in E. Scale bar = 1 mm.

Figure 2. Shh promotes the survival of TH+ neurons of the ventral mesencephalon. (A) Timecourse and dose response of the Shh effect. The number of TH+ neurons in control cultures (0 ng/ml Shh) began to decline dramatically by 5 days *in vitro*. In cultures treated with Shh at 25 and 50 ng/ml there were significantly greater numbers of TH+ neurons over control- through 24 days *in vitro* (from 5 to 24 days,  $p < .001$  at 25 and 50 ng/ml). The 50 ng/ml dose typically gave a 50-100% increase over controls at all time points (error bars s.e.m.) P-h'otomicrographs of TH+ neurons in 50 ng/ml Shh treated (B,---D) and control (C, E) cultures, 2 days (B, C) and 7 days (D, E) post-plating. Note that in addition to an increased number of TH+-cell bodies, the Shh treated cells--show extensive neuritic processes. Scale bar = 200  $\mu$ m.

Figure 3. Transport of 3H-Dopamine. The identity and functionality of the surviving midbrain neurons was assessed by their ability to specifically transport dopamine. (A) Addition of 25 ng/ml Shh resulted in a 22-fold increase in 3H-DA cell uptake over controls and lower Shh concentrations. 50 ng/ml Shh gave a 30-fold increase in 3H-DA uptake (error bars = s.d.) ( $p < 0.005$  at 25 and 50 ng/ml). (B) Autoradiography was performed on sister plates to visualize dopamine transport. Only cells with neuronal morphology transported 3H-DA (inset). Scale bar = 50  $\mu$ m, inset 15  $\mu$ m.

Figure 4. Specificity of Shh activity. (A) QC-PCR gel. Lanes 1-4 are CDNA from midbrain cultures that have been co-amplified with successive 4-fold dilutions of mimic oligo. Lane 5 is DNA marker lane. *Ptc* target is 254 bp and mimic is 100 bp (B) Representative plot (corresponding to A) of the log concentration of competitive mimic versus the log of the obtained band densities of target and mimic PCR substrates demonstrates the linearity of the amplification reaction. The extrapolated value of *ptc* message in the CDNA tested is determined to be equal to the value of mimic concentration where  $\text{Log } D_s/D_m = 0$ . See main text for details of the procedure. Doses in ng/ml;  $D_s$  = density of test substrate;  $D_m$  = density of competitive mimic. The  $r^2$  value shows that determinations made within this range vary within 3%. (C) Administration of Shh induces *ptc* expression in a dose response that parallels the survival curve. The values are expressed as number of target molecules (log  $D_s$ ) per total amount of CDNA used in each reaction as

measured by optical density at 260 nm (OD) and were determined as demonstrated in A and B. At 4 days *in vitro* Shh at 5 ng/ml increases *ptc* expression over control, and 50 ng/ml increases expression of *ptc* over the level found in the ventral mesencephalon at the time of dissection. (D) Affinity purified anti-Shh antibody inhibited the Shh neurotrophic response ( $p < .001$ ). Cultures were maintained for 5 days. Shh was added at a concentration of 50 ng/ml, and in the co-administration of 5 Shh and anti-Shh ("Shh antibody") Shh was added at 0 g/ml and anti-Shh was added as a 5-fold molar excess (error bars s.e.m.).

Figure 5. Shh also supports the survival of midbrain-GABA<sup>+</sup> neurons. (A) In addition to supporting the survival of TH<sup>+</sup> cells in the midbrain cultures, Shh promotes the survival of GABA-immunoreactive neurons with a similar dose response (error bars=s.e.m.) (For TH,  $p < 0.001$  at 25 and 50 ng/ml; for GABA,  $p < .001$  at 25 and 50 ng/ml). (B) Double level immunofluorescence of SSH-treated cultures shows that the majority of the GABA<sup>+</sup> cells (Orange) do not overlap with the TH<sup>+</sup> cells (green); scale bar = 15  $\mu$ m.

Figure 6. Shh effects on striatal cultures. (A) At concentrations of 10 ng/ml and higher, Shh promotes neuronal survival as gauged by staining for tubulin PIII, and these cells are exclusively GABA<sup>+</sup> (error bars = S.D.) (tubulin PIII,  $p < 0.001$  at 25 and 50 ng/ml; GABA,  $p < .001$  at 25 and 50 ng/ml). Typical fields of neurons treated with 50 ng/ml Shh stained for tubulin pIII (B) and GABA<sup>+</sup> (C) are shown; scale bar = 100  $\mu$ m.

Figure 7. Shh effects on ventral spinal cultures. (A) At concentrations of 25 ng/ml and higher, Shh promotes neuronal survival as gauged by staining for tubulin PIII. The majority of the cells stain positively for GABA, while a subset stain for the nuclear marker of spinal interneurons, Lim-1/2 (error bars = s.e.m.) (tubulin pIII,  $p < 0.001$  at 25 and 50 ng/ml; lim 1/2,  $p < .001$  at 5, 10, 25, and 50 ng/ml; GABA,  $p < .001$  at 25 and 50 ng/ml). Typical staining for Lim-1/2 in the E14 rat spinal cord (B, scale bar = 100  $\mu$ m), and spinal neurons cultured in the presence of 50 ng/ml Shh (C, scale bar = 20  $\mu$ m).

Figure 8. *Shh* protects midbrain TH<sup>+</sup> neurons from neurotoxic insult. Cultures of ventral mesencephalon neurons were cultured in the indicated concentrations of *Shh* (ng/ml). MPP<sup>+</sup> was added at 4 days *in vitro* for 48 hours. Cultures were then washed extensively and cultured for an additional 48 hours to allow clearance of dying neurons. Protection from MPP<sup>+</sup> neurotoxicity could be seen at 5 ng/ml, with the effect saturating at 50 ng/ml. BDNF was used at 10 ng/ml, and GDNF at 20 ng/ml (error bars = s.e.m.) (*Shh*,  $p < 0.001$  at 50 and 250 ng/ml; BDNF no significance; GDNF,  $p < .05$ ). Note that the plating density used in this experiment was twice that used in Figure 2.

Figures 9 and 10 are graphs illustrating the effects of *Shh* on apomorphine-induced rotational behavior in stably lesioned mice.

Figures 11A and 11B are graphs illustrating the neuroprotective effect of *Shh* against amphetamine challenges.

Figures 12A-B and 13A-D are graphs comparing the restorative effect of myristoylated *Shh* (Mz) and un-modified forms of *Shh* (Gz) on the rotational behavior of 6-OHDA lesioned mice.

Figures 14A-E, 15A-H and 16 are graphs illustrating the neuroprotective effect of *Shh* polypeptides against amphetamine and apomorphine challenges of 6-OHDA lesioned mice.

Figure 17 is a graph demonstrating the dose response for *hedgehog* polypeptide constructs in a malonate striatal lesion model

Figure 18 is a graph showing the effect of pretreatment with myristoylated *Shh* in a malonate striatal lesion model

### *Detailed Description of the Invention*

#### *I. Overview*

Sonic *hedgehog* (*Shh*), an axis-determining secreted protein, is expressed during early vertebrate embryogenesis in the notochord and ventral neural tube. In this site it plays a role in the phenotypic specification of ventral neurons along the length of the CNS. For example, *Shh* induces the differentiation of motor neurons in the spinal cord and dopaminergic neurons in the midbrain. *Shh* expression, however, persists beyond this induction period. We have show here that *Shh* possesses novel activities beyond phenotype specification.

Using cultures derived from the embryonic day 14.5 (E14.5) rat ventral mesencephalon, we show that *Shh* is also trophic for dopaminergic neurons. Interestingly, *Shh* not only promotes dopaminergic neuron survival, but also promotes the survival of midbrain GABA-immunoreactive (GABA-ir) neurons. In cultures derived from the E15-16 striatum, *Shh* promotes the survival of GABA-ir interneurons to the exclusion of any other cell type. Cultures derived from E15-16 ventral spinal cord reveal that *Shh* is again trophic for interneurons, many of which are GABA-ir and some of which express the Lim-1/2 nuclear marker, but does not appear to support motoneuron survival. *Shh* does not support survival of sympathetic or dorsal root ganglion neurons. Finally, using the midbrain cultures, we show that in the presence of MPP+, a highly specific neurotoxin, *Shh* prevents dopaminergic neuron death that normally would have occurred.

Moreover, as demonstrated in Examples 2-6, activation of *hedgehog* signalling pathway(s) can be used both for restoration of lesions to dopaminergic cells and other

neuronal cells of the substantia nigra (SN) and ventral termental area (VTA), as well as for neuroprotection against formation of such lesions. Briefly, as described in the appended examples, we investigated the neuroprotective and restorative potential of *hedgehog* polypeptides in various animal models of lesions involving nigrostriatal and mesolimbic dopaminergic pathways. As described in detail below, our results show that the administration of *hedgehog* polypeptide can prevent and partially restore such neuronal damage.

Furthermore, as demonstrated in the appended examples, activation of the *hedgehog* signaling pathway(s) can be a more general protective measure against neurotoxic insult, and particularly for protection against cell death due to overstimulation by excitatory amino acids.

One aspect of the present application is directed to compositions and methods for the prevention and treatment of degenerations of certain neuronal cells due to exotoxicity. The invention also specifically contemplates the use of *hedgehog* agonists for treating, preventing or ameliorating neuronal loss associated with neurologic disorders which are due to overstimulation by the excitatory amino acids. These include acute neurologic disorders such as domoic acid poisoning; spinal cord trauma; hypoglycemia; mechanical trauma to the nervous system, epileptic seizures; and chronic neurologic disorders such as Huntington's disease, neuronal injury associated with HIV and AIDS, AIDS dementia, neurodegeneration associated with Down's syndrome, neuropathic pain syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis, mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy, Tourette's syndrome, schizophrenia, and drug addiction (see Lipton and Rosenberg, N. Engl. J. Med. 330: 613-622 (1994)).

In certain preferred embodiments, the subject invention is directed to methods and compositions for preventing or ameliorating degeneration of dopaminergic cells and other neuronal cells of the substantia nigra (SN) and ventral termental area (VTA), such as resulting in Parkinson's disease. Based in part on these findings, we have determined that *Shh*, and other forms of *hedgehog* polypeptides, are useful as a protective agents in the treatment and prophylaxis for neurodegenerative disorders, particularly those resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss tissue from the substantia nigra. As described with greater detail below, exemplary disorders ("candidate disorders") include Parkinson's disease.

In one aspect, the present invention provides pharmaceutical preparations and methods for preventing/treating lesions involving exotoxic-dependent degeneration of neurons utilizing, as an active ingredient, a *hedgehog* polypeptide or a mimetic thereof.

However, without wishing to be bound by any particular theory, the protective/restorative activity of *hedgehog* polypeptides obeserved in the present studies may

be due at least in part to the ability of *hedgehog* polypeptides to antagonize (directly or indirectly) *patched*-mediated regulation of gene expression and other physiological effects mediated by the *patched* gene. The *patched* gene product, a cell surface protein, is understood to signal through a pathway which regulates transcription of a variety of genes involved in neuronal cell development. In the CNS and other tissue, the introduction of *hedgehog* relieves (derepresses) this inhibition conferred by *patched*, allowing expression of particular gene programs. Accordingly, the present invention contemplates the use of other agents which are capable of mimicking the effect of the *hedgehog* polypeptide on *patched* signalling, e.g., as may be identified from the drug screening assays described below.

The subject *hedgehog* treatments are effective on both human and animal subjects afflicted with these conditions. Animal subjects to which the invention is applicable extend to both domestic animals and livestock, raised either as pets or for commercial purposes. Examples are dogs, cats, cattle, horses, sheep, hogs and goats. In terms of treatment, once a patient experiences symptoms of a candidate disorder, a goal of therapy is prevention of further loss of neuron function.

Moreover, the subject method can also be utilized for cell culture, e.g., for the maintenance of differentiated neurons in cultures; such as in cultures of dopaminergic and GABA-nergic neurons. The subject methods and compositions can also be used to augment the implantation of such neuronal cells in an animal.

## II. Definitions

For convenience, certain terms employed in the specification, examples, and appended claims are collected here.

The term "*hedgehog* therapeutic" refers to various forms of *hedgehog* polypeptides, as well as peptidomimetics, which are neuroprotective for neuronal cells, and in particular, enhance the survival of dopaminergic and GABA-ergic neurons. These include naturally occurring forms of *hedgehog* polypeptides, as well as modified or mutant forms generated by molecular biological techniques, chemical synthesis, etc. While in preferred embodiments the *hedgehog* polypeptide is derived from a vertebrate homolog, cross-species activity reported in the literature supports the use of *hedgehog* polypeptides from invertebrate organisms as well. Naturally and non-naturally occurring *hedgehog* therapeutics referred to herein as "agonists" mimic or potentiate (collectively "agonize") the effects of a naturally-occurring *hedgehog* polypeptide as a neuroprotective agent. In addition, the term "*hedgehog* therapeutic" includes molecules which can activate expression of an endogenous *hedgehog* gene. The term also includes gene therapy constructs for causing expression of *hedgehog* polypeptides *in vivo*, as for example, expression constructs encoding recombinant *hedgehog*

polypeptides as well as trans-activation constructs for altering the regulatory sequences of an endogenous *hedgehog* gene by homologous recombination.

In particular, the term "*hedgehog* polypeptide" encompasses *hedgehog* polypeptides and peptidyl fragments thereof.

5       As used herein the term "bioactive fragment", with reference to a portions of *hedgehog* polypeptides, refers to a fragment of a full-length *hedgehog* polypeptide, wherein the fragment specifically agonizes neuroprotective events mediated by wild-type *hedgehog* polypeptides. The *hedgehog* bioactive fragment preferably is a soluble extracellular portion of a *hedgehog* polypeptide, where solubility is with reference to physiologically compatible  
10       solutions. Exemplary bioactive fragments are described in PCT publications WO 95/18856 and WO 96/17924.

      The term "*ptc* therapeutic" refers to agents which mimic the effect of naturally occurring *hedgehog* polypeptides on *patched* signalling. The *ptc* therapeutic can be, e.g., a peptide, a nucleic acid, a carbohydrate, a small organic molecule, or natural product extract  
15       (or fraction thereof).

      A "patient" or "subject" to be treated by the subject method are mammals, including humans.

      An "effective amount" of, e.g., a *hedgehog* or *ptc* therapeutic, with respect to the subject method of treatment, refers to an amount of the therapeutic in a preparation which,  
20       when applied as part of a desired dosage regimen causes a increase in survival of a neuronal cell population according to clinically acceptable standards for the treatment or prevention of a particular disorder.

      By "prevent degeneration" it is meant reduction in the loss of cells (such as from apoptosis), or reduction in impairment of cell function, e.g., release of dopamine in the case  
25       of dopaminergic neurons.

      A "trophic factor", referring to a *hedgehog* or *ptc* therapeutic, is a molecule that directly or indirectly affects the survival or function of a *hedgehog*-responsive cell, e.g., a dopaminergic or GABAergic cell.

      A "trophic amount" of a a *hedgehog* or *ptc* therapeutic is an amount sufficient to,  
30       under the circumstances, cause an increase in the rate of survival or the functional performance of a *hedgehog*-responsive cell, e.g., a dopaminergic or GABAergic cell.

      "Homology" and "identity" each refer to sequence similarity between two polypeptide sequences, with identity being a more strict comparison. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of  
35       comparison. When a position in the compared sequence is occupied by the same amino acid

residue, then the polypeptides can be referred to as identical at that position; when the equivalent site is occupied by the same amino acid (e.g., identical) or a similar amino acid (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous at that position. A percentage of homology or identity between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40 percent identity, though preferably less than 25 percent identity, with a hedgehog sequence.

In particular, the term "percent identical" refers to sequence identity between two amino acid sequences or between two nucleotide sequences. Identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology/similarity or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. Various alignment algorithms and/or programs may be used, including FASTA, BLAST or ENTREZ. FASTA and BLAST are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with, e.g., default settings. ENTREZ is available through the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, Md. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences.

The term "corresponds to", when referring to a particular polypeptide or nucleic acid sequence is meant to indicate that the sequence of interest is identical or homologous to the reference sequence to which it is said to correspond.

The terms "recombinant protein", "heterologous protein" and "exogenous protein" are used interchangeably throughout the specification and refer to a polypeptide which is produced by recombinant DNA techniques, wherein generally, DNA encoding the polypeptide is inserted into a suitable expression construct which is in turn used to transform a host cell to produce the heterologous protein. That is, the polypeptide is expressed from a heterologous nucleic acid.

A "chimeric protein" or "fusion protein" is a fusion of a first amino acid sequence encoding a *hedgehog* polypeptide with a second amino acid sequence defining a domain foreign to and not substantially homologous with any domain of *hh* protein. A chimeric protein may present a foreign domain which is found (albeit in a different protein) in an



organism which also expresses the first protein, or it may be an "interspecies", "intergenic", etc. fusion of protein structures expressed by different kinds of organisms. In general, a fusion protein can be represented by the general formula  $(X)_n-(hh)_m-(Y)_n$ , wherein *hh* represents all or a portion of the *hedgehog* polypeptide, X and Y each independently represent an amino acid sequences which are not naturally found as a polypeptide chain contiguous with the *hedgehog* sequence, m is an integer greater than or equal to 1, and each occurrence of n is, independently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. The term "expression vector" includes plasmids, cosmids or phages capable of synthesizing, for example, the subject *hedgehog* polypeptides encoded by the respective recombinant gene carried by the vector. Preferred vectors are those capable of autonomous replication and/expression of nucleic acids to which they are linked. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. Moreover, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

"Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, as well as polyadenylation sites, which induce or control transcription of protein (or antisense) coding sequences with which they are operably linked. In preferred embodiments, transcription of a recombinant gene is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring form of the regulatory protein.

The term "operably linked" refers to the arrangement of a transcriptional regulatory element relative to other transcribable nucleic acid sequence such that the transcriptional regulatory element can regulate the rate of transcription from the transcribable sequence(s).

### *III. Exemplary Applications of Method and Compositions*

One aspect of the present invention relates to a method of maintaining a differentiated state, e.g., enhancing survival, of a neuronal cell responsive to a *hedgehog* polypeptide, by contacting the cells with a trophic amount of a *hedgehog* or *ptc* thereapeutic. For instance, it is contemplated by the invention that, in light of the present finding of an apparently trophic

effect of *hedgehog* polypeptides in the maintenance of differentiated neurons, the subject method could be used to maintain different neuronal tissue both *in vitro* and *in vivo*. Where the trophic agent is a *hedgehog* polypeptide, it can be provided to a cell culture or animal as a purified protein or secreted by a recombinant cell, or cells or tissue explants which naturally produce one or more *hedgehog* polypeptides. For instance, neural tube explants from embryos, particularly floorplate tissue, can provide a source for *Shh* polypeptide, which source can be implanted in a patient or otherwise provided, as appropriate, for maintenance of differentiation.

#### A. Cell Culture

The present method is applicable to cell culture techniques. *In vitro* neuronal culture systems have proved to be fundamental and indispensable tools for the study of neural development, as well as the identification of neurotrophic factors such as nerve growth factor (NGF), ciliary trophic factors (CNTF), and brain derived neurotrophic factor (BDNF). Once a neuronal cell has become terminally-differentiated it typically will not change to another terminally differentiated cell-type. However, neuronal cells can nevertheless readily lose their differentiated state. This is commonly observed when they are grown in culture from adult tissue, and when they form a blastema during regeneration. The present method provides a means for ensuring an adequately restrictive environment in order to maintain dopaminergic, GABAergic or other exotoxic-sensitive neuronal cells in differentiated states, and can be employed, for instance, in cell cultures designed to test the specific activities of other trophic factors.

In such embodiments of the subject method, a culture of differentiated cells including the neuronal cells can be contacted with a *hedgehog* or *ptc* therapeutic in order to maintain the integrity of a culture of terminally-differentiated neuronal cells by preventing loss of differentiation. The source of *hedgehog* or *ptc* therapeutic in the culture can be derived from, for example, a purified or semi-purified protein composition added directly to the cell culture media, or alternatively, supported and/or released from a polymeric device which supports the growth of various neuronal cells and which has been doped with the protein. The source of, for example, a trophic *hedgehog* polypeptide can also be a cell that is co-cultured with the neuronal cells. Alternatively, the source can be the neuronal cell itself which has been engineered to produce a recombinant *hedgehog* polypeptide. Such neuronal cultures can be used as convenient assay systems as well as sources of implantable cells for therapeutic treatments.

The subject method can be used in conjunction with agents which induce the differentiation of neuronal precursors, e.g., progenitor or stem cells, into dopaminergic neurons, GABAergic neurons or other neuronal cell-types.

Cells can be obtained from embryonic, post-natal, juvenile or adult neural tissue from any animal. By any animal is meant any multicellular animal which contains nervous tissue. More particularly, is meant any fish, reptile, bird, amphibian or mammal and the like. The most preferable donors are mammals, especially humans and non-human primates, pigs, cows, and rodents.

Intracerebral neural grafting has emerged recently as an additional potential to CNS therapy. For example, one approach to repairing damaged brain tissues involves the transplantation of cells from fetal or neonatal animals into the adult brain (Dunnett et al. (1987) *J Exp Biol* 123:265-289; and Freund et al. (1985) *J Neurosci* 5:603-616). Fetal neurons from a variety of brain regions can be successfully incorporated into the adult brain, and such grafts can alleviate behavioral defects. For example, movement disorder induced by lesions of dopaminergic projections to the basal ganglia can be prevented by grafts of embryonic dopaminergic neurons. Complex cognitive functions that are impaired after lesions of the neocortex can also be partially restored by grafts of embryonic cortical cells. Transplantation of fetal brain cells, which contain precursors of the dopaminergic neurons, has been examined with success as a treatment for Parkinson's disease. In animal models and in patients with this disease, fetal brain cell transplantations have resulted in the reduction of motor abnormalities. Furthermore, it appears that the implanted fetal dopaminergic neurons form synapses with surrounding host neurons. However, in the art, the transplantation of fetal brain cells is limited due, for example, to the limited survival time of the implanted neuronal precursors and differentiated neurons arising therefrom. The subject invention provides a means for extending the usefulness of such transplants by enhancing the survival of dopaminergic and/or GABAergic cells in the transplant.

In the specific case of Parkinson's disease, intervention by increasing the activity of *hedgehog*, by ectopic or endogenous means, can improve the *in vivo* survival of fetal and adult dopaminergic neurons, and thus can provide a more effective treatment of this disease. Cells to be transplanted for the treatment of a particular disease can be genetically modified *in vitro* so as to increase the expression of *hedgehog* in the transplant. In an exemplary embodiment of the invention, administration of an *Shh* polypeptide can be used in conjunction with surgical implantation of tissue in the treatment of Parkinson's disease.

In the case of a heterologous donor animal, the animal may be euthanized, and the brain and specific area of interest removed using a sterile procedure. Brain areas of particular interest include any area from which progenitor cells can be obtained which will provide dopaminergic or GABAergic cells upon differentiation. These regions include areas of the central nervous system (CNS) including the substantia nigra pars compacta which is found to be degenerated in Parkinson's Disease patients.

Human heterologous neural progenitor cells may be derived from fetal tissue obtained from elective abortion, or from a post-natal, juvenile or adult organ donor. Autologous neural tissue can be obtained by biopsy, or from patients undergoing neurosurgery in which neural tissue is removed, such as during epilepsy surgery.

5 Cells can be obtained from donor tissue by dissociation of individual cells from the connecting extracellular matrix of the tissue. Dissociation can be obtained using any known procedure, including treatment with enzymes such as trypsin, collagenase and the like, or by using physical methods of dissociation such as with a blunt instrument. Dissociation of fetal cells can be carried out in tissue culture medium, while a preferable medium for dissociation  
10 of juvenile and adult cells is artificial cerebral spinal fluid (aCSF). Regular aCSF contains 124 mM NaCl, 5 mM KCl, 1.3 mM MgCl<sub>2</sub>, 2 mM CaCl<sub>2</sub>, 26 mM NaHCO<sub>3</sub>, and 10 mM D-glucose. Low Ca<sup>2+</sup> aCSF contains the same ingredients except for MgCl<sub>2</sub> at a concentration of 3.2 mM and CaCl<sub>2</sub> at a concentration of 0.1 mM.

Dissociated cells can be placed into any known culture medium capable of supporting  
15 cell growth, including MEM, DMEM, RPMI, F-12, and the like, containing supplements which are required for cellular metabolism such as glutamine and other amino acids, vitamins, minerals and useful proteins such as transferrin and the like. Medium may also contain antibiotics to prevent contamination with yeast, bacteria and fungi such as penicillin, streptomycin, gentamicin and the like. In some cases, the medium may contain serum  
20 derived from bovine, equine, chicken and the like. A particularly preferable medium for cells is a mixture of DMEM and F-12.

Conditions for culturing should be close to physiological conditions. The pH of the culture media should be close to physiological pH, preferably between pH 6-8, more preferably close to pH 7, even more particularly about pH 7.4. Cells should be cultured at  
25 temperature close to physiological temperature, preferably between 30°C-40°C, more preferably between 32°C-38°C, and most preferably between 35°C-37°C.

Cells can be grown in suspension or on a fixed substrate, but proliferation of the progenitors is preferably done in suspension to generate large numbers of cells by formation of "neurospheres" (see, for example, Reynolds et al. (1992) *Science* 255:1070-1709; and PCT  
30 Publications WO93/01275, WO94/09119, WO94/10292, and WO94/16718). In the case of propagating (or splitting) suspension cells, flasks are shaken well and the neurospheres allowed to settle on the bottom corner of the flask. The spheres are then transferred to a 50 ml centrifuge tube and centrifuged at low speed. The medium is aspirated, the cells resuspended in a small amount of medium with growth factor, and the cells mechanically  
35 dissociated and resuspended in separate aliquots of media.

Cell suspensions in culture medium are supplemented with any growth factor which allows for the proliferation of progenitor cells and seeded in any receptacle capable of sustaining cells, though as set out above, preferably in culture flasks or roller bottles. Cells typically proliferate within 3-4 days in a 37°C incubator, and proliferation can be reinitiated at any time after that by dissociation of the cells and resuspension in fresh medium containing growth factors.

In the absence of substrate, cells lift off the floor of the flask and continue to proliferate in suspension forming a hollow sphere of undifferentiated cells. After approximately 3-10 days *in vitro*, the proliferating clusters (neurospheres) are fed every 2-7 days, and more particularly every 2-4 days by gentle centrifugation and resuspension in medium containing growth factor.

After 6-7 days *in vitro*, individual cells in the neurospheres can be separated by physical dissociation of the neurospheres with a blunt instrument, more particularly by triturating the neurospheres with a pipette. Single cells from the dissociated neurospheres are suspended in culture medium containing growth factors, and differentiation of the cells can be induced by plating (or resuspending) the cells in the presence of a factor capable of sustaining differentiation, e.g., such as a *hedgehog* or *ptc* therapeutic of the present invention.

Stem cells useful in the present invention are generally known. For example, several neural crest cells have been identified, some of which are multipotent and likely represent uncommitted neural crest cells. The role of *hedgehog* polypeptides employed in the present method to culture such stem cells is to maintain differentiation a committed progenitor cell and/or a terminally-differentiated dopaminergic or GABAergic neuronal cell. The *hedgehog* polypeptide can be used alone, or can be used in combination with other neurotrophic factors which act to more particularly enhance a particular differentiation fate of the neuronal progenitor cell.

#### B. In vivo applications

In addition to the implantation of cells cultured in the presence of a functional *hedgehog* activity and other *in vitro* uses described above, yet another aspect of the present invention concerns the therapeutic application of a *hedgehog* or *ptc* therapeutic to enhance survival of neurons sensitive to exotoxic degeneration *in vivo*, e.g., such as dopaminergic and GABAergic neurons. The ability of *hedgehog* polypeptide to maintain neuronal differentiation indicates that certain of the *hedgehog* polypeptides can be reasonably expected to facilitate control of these neuronal cell-types in adult tissue with regard to maintenance, functional performance, aging and prevention of degeneration and premature death which result from loss of differentiation in certain pathological conditions.

In light of this understanding, the present invention specifically contemplates applications of the subject method to the treatment of (prevention and/or reduction of the severity of) neurological conditions deriving from exotoxic degeneration of neuronal cells, including cell death or loss of functional performance, e.g., such as loss of dopaminergic cells, loss of GABAergic cells, and/or loss of neurons of the substantia nigra. In this regard, the subject method is useful in the treatment or prevention of such neurologic disorders including Parkinson's disease, domoic acid poisoning; spinal cord trauma; hypoglycemia; mechanical trauma to the nervous system; senile dementia; Korsakoff's disease; schizophrenia; AIDS dementia, multi-infarct dementia; mood disorders; depression; chemical toxicity and neuronal damage associated with uncontrolled seizures, such as epileptic seizures; and chronic neurologic disorders such as Huntington's disease, neuronal injury associated with HIV and AIDS, AIDS dementia, neurodegeneration associated with Down's syndrome, neuropathic pain syndrome, olivopontocerebral atrophy, amyotrophic lateral sclerosis, mitochondrial abnormalities, Alzheimer's disease, hepatic encephalopathy, Tourette's syndrome, schizophrenia, and drug addiction.

The subject *hedgehog* and *ptc* therapeutics can also be used to reduce neurotoxic injury associated with conditions of hypoxia, anoxia or ischemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drownings, suffocation, perinatal asphyxia, or hypoglycemic events.

In preferred embodiments, the subject method is used to reduce the severity or prevent Parkinson's disease or Huntington's chorea.

In general, the therapeutic method of the present invention can be characterized as including a step of administering to an animal an amount of a *ptc* or *hedgehog* therapeutic effective to enhance the survival of a dopaminergic and/or GABAergic neuronal cells. The mode of administration and dosage regimens will vary depending on the severity of the degenerative disorder being treated, e.g., the dosage may be altered as between a prophylaxis and treatment. In preferred embodiments, the *ptc* or *hedgehog* therapeutic is administered systemically initially, then locally for medium to long term care. In certain embodiments, a source of a *hedgehog* or *ptc* therapeutic is stereotactically provided within or proximate the area of degeneration.

The subject method may also find particular utility in treating or preventing the adverse neurological consequences of surgery. For example, certain cranial surgery can result in degeneration of neuronal populations for which the subject method can be applied.

In other embodiments, the subject method can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, such as the compound MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine).

In still other embodiments, the subject method can be used in the prevention and/or treatment of hypoxia, e.g., as a neuroprotective agent. For instance, the subject method can be used prophylactically to lessen the neuronal cell death caused by altitude-induced hypoxia.

5 A method which is "neuroprotective", in the case of dopaminergic and GABAergic cells, results in diminished loss of cells of those phenotype relative to that which would occur in the absence of treatment with a *hedgehog* or *ptc* therapeutic.

(i) *Treatment of Parkinson's disease*

10 It is now widely appreciated that the primary pathology underlying Parkinson's disease is degeneration of the dopaminergic projection from the substantia nigra to the striatum. This realisation has led to the widespread use of dopamine-replacing agents such as L-DOPA and apomorphine as symptomatic treatments for Parkinson's disease. Over the last three decades, such therapies have undoubtedly been successful in increasing the quality of life of patients suffering from Parkinson's disease, but, dopamine-replacement treatments do have limitations, especially following long-term treatment. Problems can include a wearing-off of anti-parkinsonian efficacy and the appearance of a range of dyskinesias characterised by chorea and dystonia. Ultimately, these side-effects can severely limit the usefulness of dopaminergic treatments.

20 As described in the appended examples, *hedgehog* exerts trophic and survival-promoting actions on substantia nigra dopaminergic neurons. *In vivo*, treatment with exogenous *hedgehog*, or other compounds of the present invention, is expected to stimulate, for example, the dopaminergic phenotype of substantia nigra neurons and restore functional deficits induced by axotomy or dopaminergic neurotoxins. Therefore it may be used in the treatment of Parkinson's disease, a neurodegenerative disease characterized by the loss of dopaminergic neurons. Thus, in one embodiment, the subject method comprises administering to an animal afflicted with Parkinson's disease, or at risk of developing Parkinson's disease, an amount of a *hedgehog* or *ptc* therapeutic effective for protecting or restoring the function of neurons affected by the Parkinson's condition, e.g., increasing the rate of survival of dopaminergic neurons in the animal. In preferred embodiments, the method includes administering to the animal an amount of a *hedgehog* or *ptc* therapeutic which would otherwise be effective at protecting the substantia nigra from MPTP-mediated toxicity when MPTP is administered at a dose of .5mg/kg, more preferably at a dose of 2mg/kg, 5mg/kg, 10mg/kg, 20mg/kg or 50mg/kg and, more preferably, at a dose of 100mg/kg.

(ii) *Treatment of Huntington's disease*

Huntington's disease involves the degeneration of intrastriatal and cortical cholinergic neurons and GABAergic neurons. Treatment of patients suffering from such degenerative conditions can include the application of *hedgehog* or *ptc* therapeutics of the present invention, in order to control, for example, apoptotic events which give rise to loss of  
5 GABAergic neurons (e.g. to enhance survival of existing neurons).

*(iii) Treatment of amyotrophic lateral sclerosis*

Recently it has been reported that in certain ALS patients and animal models a significant loss of midbrain dopaminergic neurons occurs in addition to the loss of spinal motor neurons. For instance, the literature describes degeneration of the substantia nigra in  
10 some patients with familial amyotrophic lateral sclerosis. Kostic et al. (1997) Ann Neurol 41:497-504. According to the subject invention, a trophic amount of a *hedgehog* or *ptc* therapeutic can be administered to an animal suffering from, or at risk of developing, ALS.

*(iv) Treatment of epilepsy*

Epilepsy is a recurrent paroxysmal disorder of cerebral function characterized by  
15 sudden brief attacks of altered consciousness, motor activity, sensory phenomena or inappropriate behavior caused by abnormal excessive discharge of cerebral neurons. Convulsive seizures, the most common form of attacks, begin with loss of consciousness and motor control, and tonic or clonic jerking of all extremities but any recurrent seizure pattern may be termed epilepsy.

20 The term primary or idiopathic epilepsy denotes those cases where no cause for the seizures can be identified. Secondary or symptomatic epilepsy designates the disorder when it is associated with such factors as trauma, neoplasm, infection, developmental abnormalities, cerebrovascular disease, or various metabolic conditions. Epileptic seizures are classified as partial seizures (focal, local seizures) or generalized seizures (convulsive or nonconvulsive).  
25 Classes of partial seizures include simple partial seizures, complex partial seizures and partial seizures secondarily generalized. Classes of generalized seizures include absence seizures, atypical absence seizures, myoclonic seizures, clonic seizures, tonic seizures, tonic-clonic seizures (grand mal) and atonic seizures.

Therapeutics having anticonvulsant properties are used in the treatment of seizures.  
30 Most therapeutics used to abolish or attenuate seizures act at least through effects that reduce the spread of excitation from seizure foci and prevent detonation and disruption of function of normal aggregates of neurons. Anticonvulsants which have been utilized include phenytoin, phenobarbital, primidone, carbamazepine, ethosuximide, clonazepam and valproate. For further details of seizures and their therapy (see Rall & Schleifer (1985) and The Merck  
35 Manual (1992)).



Due to the involvement of excitotoxic-dependent neurodegeneration which can result from seizure, certain *hedgehog* and *ptc* therapeutics of the present invention may be useful as part of a regimen in the treatment of epilepsy, and are preferably used in conjunction with a treatment including an anticonvulsant agent.

5           (v) *Treatment of reperfusion injury*

The most direct approach to treating cerebral ischemia is to restore circulation. However, reperfusion following transient ischemia can induce additional mechanisms of tissue damage. This phenomenon is termed "reperfusion injury" and has been found to play a role in other organ systems as well, including the heart. Recently, it has been suggested that cerebral ischemic damage is mediated, to a large extent, via excitotoxic mechanisms. During ischemia, large elevations in extracellular glutamate occur, often reaching neurotoxic levels. Accordingly, the subject method can be used as part of a treatment or prophylaxis for ischemic or excitotoxic damage, particularly to alleviate certain effects of reperfusion injury.

          (vi) *Treatment of glaucoma*

15           Glaucoma is a complex set of diseases, which results in damage to axons in the optic nerve and death of the retinal ganglion cells, concluding in the permanent loss of vision. There are several mechanism that ultimately causes the axonal damage. For instance, an increase in intraocular pressure (IOP) overcomes the perfusion pressure of the optic nerve and results in an ischemic event which leads to axonal.

20           In addition to the primary insult and ensuing cell damage, there appears to be a secondary degenerative process in glaucoma. Clinically, patients often continue to lose visual field and optic nerve head substance even in the presence of what might be considered normal IOP. In addition, there are forms of glaucoma which manifest in the presence of normal IOP. It is thought that chemical mediators may be linked to intensification of cell degeneration and death in a secondary fashion. Much work has been done in the last five years which implicates the role of excitotoxins, such as glutamate, in the secondary damage to retinal neurons. Accordingly, the subject method can be used as part of a treatment and/or prophylaxis for glaucoma.

          (vii) *Treatment of hearing loss*

30           The mechanism by which aminoglycosides produce permanent hearing loss is mediated, in part, through an excitotoxic process. Accordingly, the subject method can be used as part of a treatment and/or prophylaxis for hearing loss.

(viii) *Conjoint Therapy*

In yet other embodiments, the subject method can be carried out conjointly with the administration of growth and/or trophic factors. For instance, the combinatorial therapy can include a trophic factor such as nerve growth factor, ciliary neurotrophic growth factor, 5 schwanoma-derived growth factor, glial growth factor, stiatal-derived neuronotrophic factor, platelet-derived growth factor, and scatter factor (HGF-SF). Antimitogenic agents can also be used, as for example, cytosine, arabinoside, 5-fluorouracil, hydroxyurea, and methotrexate.

(ix) *Formulations*

Determination of a therapeutically effective amount and a prophylactically effective 10 amount of a *hedgehog* or *ptc* therapeutic, e.g., to be adequately neuroprotective, can be readily made by the physician or veterinarian (the "attending clinician"), as one skilled in the art, by the use of known techniques and by observing results obtained under analogous circumstances. The dosages may be varied depending upon the requirements of the patient in the judgment of the attending clinician, the severity of the condition being treated, the risk of 15 further degeneration to the CNS, and the particular agent being employed. In determining the therapeutically effective trophic amount or dose, and the prophylactically effective amount or dose, a number of factors are considered by the attending clinician, including, but not limited to: the specific cause of the degenerative state and its likelihood of recurring or worsening; pharmacodynamic characteristics of the particular agent and its mode and route of 20 administration; the disorder time course of treatment; the species of mammal; its size, age, and general health; the response of the individual patient; the particular compound administered; the bioavailability characteristics of the preparation administered; the dose regimen selected; the kind of concurrent treatment (i.e., the interaction of the *hedgehog* or *ptc* therapeutic with other co-administered therapeutics); and other relevant circumstances.

25 Treatment can be initiated with smaller dosages which are less than the optimum dose of the agent. Thereafter, the dosage should be increased by small increments until the optimum effect under the circumstances is reached. For convenience, the total daily dosage may be divided and administered in portions during the day if desired. A therapeutically effective trophic amount and a prophylactically effective neuroprotective amount of a 30 *hedgehog* polypeptide, for instance, is expected to vary from concentrations about 0.1 nanogram per kilogram of body weight per day (ng/kg/day) to about 100 mg/kg/day.

Potential *hedgehog* and *ptc* therapeutics, such as described below, can be tested by any of number of well known animal disease models. For instance, regarding Parkinson's Disease, selected agents can be evaluated in animals treated with MPTP. The compound 35 MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine) and its metabolite MPP<sup>+</sup> have been used to induce experimental parkinsonism. MPP<sup>+</sup> kills dopaminergic neurons in the

substantia nigra, yielding a reasonable model of late parkinsonism. Turski et al., (1991) *Nature* 349:414.

Compounds which are determined to be effective for the prevention or treatment of degeneration of dopaminergic and GABAergic neurons and the like in animals, e.g., dogs, rodents, may also be useful in treatment of disorders in humans. Those skilled in the art of treating in such disorders in humans will be guided, from the data obtained in animal studies, to the correct dosage and route of administration of the compound to humans. In general, the determination of dosage and route of administration in humans is expected to be similar to that used to determine administration in animals.

The identification of those patients who are in need of prophylactic treatment for disorders marked by degeneration of dopaminergic and/or GABAergic neurons is well within the ability and knowledge of one skilled in the art. Certain of the methods for identification of patients which are at risk and which can be treated by the subject method are appreciated in the medical arts, such as family history of the development of a particular disease state and the presence of risk factors associated with the development of that disease state in the subject patient. A clinician skilled in the art can readily identify such candidate patients, by the use of, for example, clinical tests, physical examination and medical/family history.

#### *IV. Exemplary hedgehog therapeutic compounds.*

The *hedgehog* therapeutic compositions of the subject method can be generated by any of a variety of techniques, including purification of naturally occurring proteins, recombinantly produced proteins and synthetic chemistry. Polypeptide forms of the *hedgehog* therapeutics are preferably derived from vertebrate *hedgehog* polypeptides, e.g., have sequences corresponding to naturally occurring *hedgehog* polypeptides, or fragments thereof, from vertebrate organisms. However, it will be appreciated that the *hedgehog* polypeptide can correspond to a *hedgehog* polypeptide (or fragment thereof) which occurs in any metazoan organism.

The various naturally-occurring *hedgehog* polypeptides from which the subject therapeutics can be derived are characterized by a signal peptide, a highly conserved N-terminal region, and a more divergent C-terminal domain. In addition to signal sequence cleavage in the secretory pathway (Lee, J.J. et al. (1992) *Cell* 71:33-50; Tabata, T. et al. (1992) *Genes Dev.* 2635-2645; Chang, D.E. et al. (1994) *Development* 120:3339-3353), *hedgehog* precursor proteins naturally undergo an internal autoproteolytic cleavage which depends on conserved sequences in the C-terminal portion (Lee et al. (1994) *Science* 266:1528-1537; Porter et al. (1995) *Nature* 374:363-366). This autocleavage leads to a 19 kD N-terminal peptide and a C-terminal peptide of 26-28 kD (Lee et al. (1992) *supra*; Tabata et

al. (1992) *supra*; Chang *et al.* (1994) *supra*; Lee *et al.* (1994) *supra*; Bumcrot, D.A., *et al.* (1995) *Mol. Cell. Biol.* 15:2294-2303; Porter *et al.* (1995) *supra*; Ekker, S.C. *et al.* (1995) *Curr. Biol.* 5:944-955; Lai, C.J. *et al.* (1995) *Development* 121:2349-2360). The N-terminal peptide stays tightly associated with the surface of cells in which it was synthesized, while the

5 C-terminal peptide is freely diffusible both *in vitro* and *in vivo* (Lee *et al.* (1994) *supra*; Bumcrot *et al.* (1995) *supra*; Mart', E. *et al.* (1995) *Development* 121:2537-2547; Roelink, H. *et al.* (1995) *Cell* 81:445-455). Cell surface retention of the N-terminal peptide is dependent on autocleavage, as a truncated form of *hedgehog* encoded by an RNA which terminates

10 precisely at the normal position of internal cleavage is diffusible *in vitro* (Porter *et al.* (1995) *supra*) and *in vivo* (Porter, J.A. *et al.* (1996) *Cell* 86, 21-34). Biochemical studies have shown that the autoproteolytic cleavage of the *hedgehog* precursor protein proceeds through an internal thioester intermediate which subsequently is cleaved in a nucleophilic substitution. It is suggested that the nucleophile is a small lipophilic molecule, more particularly cholesterol, which becomes covalently bound to the C-terminal end of the N-

15 peptide (Porter *et al.* (1996) *supra*), tethering it to the cell surface.

The vertebrate family of *hedgehog* genes includes at least four members, e.g., paralogs of the single drosophila *hedgehog* gene (SEQ ID No. 19). Three of these members, herein referred to as Desert *hedgehog* (*Dhh*), Sonic *hedgehog* (*Shh*) and Indian *hedgehog* (*Ihh*), apparently exist in all vertebrates, including fish, birds, and mammals. A fourth

20 member, herein referred to as tiggie-winkle *hedgehog* (*Thh*), appears specific to fish. According to the appended sequence listing, (see also Table 1) a chicken *Shh* polypeptide is encoded by SEQ ID No:1; a mouse *Dhh* polypeptide is encoded by SEQ ID No:2; a mouse *Ihh* polypeptide is encoded by SEQ ID No:3; a mouse *Shh* polypeptide is encoded by SEQ ID No:4 a zebrafish *Shh* polypeptide is encoded by SEQ ID No:5; a human *Shh* polypeptide is

25 encoded by SEQ ID No:6; a human *Ihh* polypeptide is encoded by SEQ ID No:7; a human *Dhh* polypeptide is encoded by SEQ ID No. 8; and a zebrafish *Thh* is encoded by SEQ ID No. 9.

Table 1  
Guide to *hedgehog* sequences in Sequence Listing

	Nucleotide	Amino Acid
Chicken <i>Shh</i>	SEQ ID No. 1	SEQ ID No. 10
Mouse <i>Dhh</i>	SEQ ID No. 2	SEQ ID No. 11
Mouse <i>Ihh</i>	SEQ ID No. 3	SEQ ID No. 12
Mouse <i>Shh</i>	SEQ ID No. 4	SEQ ID No. 13
Zebrafish <i>Shh</i>	SEQ ID No. 5	SEQ ID No. 14
Human <i>Shh</i>	SEQ ID No. 6	SEQ ID No. 15
Human <i>Ihh</i>	SEQ ID No. 7	SEQ ID No. 16
Human <i>Dhh</i>	SEQ ID No. 8	SEQ ID No. 17
Zebrafish <i>Thh</i>	SEQ ID No. 9	SEQ ID No. 18
Drosophila <i>HH</i>	SEQ ID No. 19	SEQ ID No. 20

In addition to the sequence variation between the various *hedgehog* homologs, the *hedgehog* polypeptides are apparently present naturally in a number of different forms, including a pro-form, a full-length mature form, and several processed fragments thereof.

5 The pro-form includes an N-terminal signal peptide for directed secretion of the extracellular domain, while the full-length mature form lacks this signal sequence.

As described above, further processing of the mature form occurs in some instances to yield biologically active fragments of the protein. For instance, *sonic hedgehog* undergoes additional proteolytic processing to yield two peptides of approximately 19 kDa and 27 kDa,

10 the 19kDa fragment corresponding to an proteolytic N-terminal portion of the mature protein.

In addition to proteolytic fragmentation, the vertebrate *hedgehog* polypeptides can also be modified post-translationally, such as by glycosylation and/or addition of lipophilic moieties, such as stents, fatty acids, etc., though bacterially produced (e.g. unmodified) forms of the proteins still maintain certain of the bioactivities of the native protein. Bioactive

15 fragments of *hedgehog* polypeptides of the present invention have been generated and are described in great detail in, e.g., PCT publications WO 95/18856 and WO 96/17924.

There are a wide range of lipophilic moieties with which *hedgehog* polypeptides can be derivatized. The term "lipophilic group", in the context of being attached to a *hedgehog* polypeptide, refers to a group having high hydrocarbon content thereby giving the group high

20 affinity to lipid phases. A lipophilic group can be, for example, a relatively long chain alkyl or cycloalkyl (preferably n-alkyl) group having approximately 7 to 30 carbons. The alkyl group may terminate with a hydroxy or primary amine "tail". To further illustrate, lipophilic molecules include naturally-occurring and synthetic aromatic and non-aromatic moieties such as fatty acids, sterols, esters and alcohols, other lipid molecules, cage structures such as

25 adamantane and buckminsterfullerenes, and aromatic hydrocarbons such as benzene, perylene, phenanthrene, anthracene, naphthalene, pyrene, chrysene, and naphthacene.

In one embodiment, the *hedgehog* polypeptide is modified with one or more sterol moieties, such as cholesterol. See, for example, PCT publication WO 96/17924. In certain embodiments, the cholesterol is preferably added to the C-terminal glycine when the

30 *hedgehog* polypeptide corresponds to the naturally-occurring N-terminal proteolytic fragment.

In another embodiment, the *hedgehog* polypeptide can be modified with a fatty acid moiety, such as a myrostoyl, palmitoyl, stearoyl, or arachidoyl moiety. See, e.g., Pepinsky et al. (1998) J Biol. Chem 273: 14037.

35 In addition to those effects seen by cholesterol-addition to the C-terminus or fatty acid addition to the N-terminus of extracellular fragments of the protein, at least certain of the

biological activities of the *hedgehog* gene products are unexpectedly potentiated by derivatization of the protein with lipophilic moieties at other sites on the protein and/or by moieties other than cholesterol or fatty acids. Certain aspects of the invention are directed to the use of preparations of *hedgehog* polypeptides which are modified at sites other than N-terminal or C-terminal residues of the natural processed form of the protein, and/or which are modified at such terminal residues with lipophilic moieties other than a sterol at the C-terminus or fatty acid at the N-terminus.

Particularly useful as lipophilic molecules are alicyclic hydrocarbons, saturated and unsaturated fatty acids and other lipid and phospholipid moieties, waxes, cholesterol, isoprenoids, terpenes and polyalicyclic hydrocarbons including adamantane and buckminsterfullerenes, vitamins, (C1-C18)-alkyl phosphate diesters, -O-CH<sub>2</sub>-CH(OH)-O-(C12-C18)-alkyl, and in particular conjugates with pyrene derivatives. The lipophilic moiety can be a lipophilic dye suitable for use in the invention include, but are not limited to, diphenylhexatriene, Nile Red, N-phenyl-1-naphthylamine, Prodan, Laurodan, Pyrene, Perylene, rhodamine, rhodamine B, tetramethylrhodamine, Texas Red, sulforhodamine, 1,1'-didodecyl-3,3',3',3'tetramethylindocarbocyanine perchlorate, octadecyl rhodamine B and the BODIPY dyes available from Molecular Probes Inc.

Other exemplary lipophilic moieties include aliphatic carbonyl radical groups include 1- or 2-adamantylacetyl, 3-methyladamant-1-ylacetyl, 3-methyl-3-bromo-1-adamantylacetyl, 1-decalinacetyl, camphoracetyl, camphaneacetyl, noradamantylacetyl, norbornaneacetyl, bicyclo[2.2.2.]-oct-5-eneacetyl, 1-methoxybicyclo[2.2.2.]-oct-5-ene-2-carbonyl, cis-5-norbornene-endo-2,3-dicarbonyl, 5-norbornen-2-ylacetyl, (1R)-( - )-myrtentaneacetyl, 2-norbornaneacetyl, anti-3-oxo-tricyclo[2.2.1.0<2,6>]-heptane-7-carbonyl, decanoyl, dodecanoyl, dodecenoyl, tetradecadienoyl, decynoyl or dodecynoyl.

The *hedgehog* polypeptide can be linked to the hydrophobic moiety in a number of ways including by chemical coupling means, or by genetic engineering.

There are a large number of chemical cross-linking agents that are known to those skilled in the art. For the present invention, the preferred cross-linking agents are heterobifunctional cross-linkers, which can be used to link the *hedgehog* polypeptide and hydrophobic moiety in a stepwise manner. Heterobifunctional cross-linkers provide the ability to design more specific coupling methods for conjugating to proteins, thereby reducing the occurrences of unwanted side reactions such as homo-protein polymers. A wide variety of heterobifunctional cross-linkers are known in the art. These include: succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC), m-Maleimidobenzoyl-N-hydroxysuccinimide ester (MBS); N-succinimidyl (4-iodoacetyl) aminobenzoate (SIAB), succinimidyl 4-(p-maleimidophenyl) butyrate (SMPB), 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC); 4-succinimidylloxycarbonyl- $\alpha$ -methyl- $\alpha$ -(2-

pyridyldithio)-tolune (SMPT), N-succinimidyl 3-(2-pyridyldithio) propionate (SPDP), succinimidyl 6-[3-(2-pyridyldithio) propionate] hexanoate (LC-SPDP). Those cross-linking agents having N-hydroxysuccinimide moieties can be obtained as the N-hydroxysulfosuccinimide analogs, which generally have greater water solubility. In addition, those cross-linking agents having disulfide bridges within the linking chain can be synthesized instead as the alkyl derivatives so as to reduce the amount of linker cleavage *in vivo*.

In addition to the heterobifunctional cross-linkers, there exists a number of other cross-linking agents including homobifunctional and photoreactive cross-linkers. Disuccinimidyl suberate (DSS), bismaleimido-hexane (BMH) and dimethylpimelimidate-2 HCl (DMP) are examples of useful homobifunctional cross-linking agents, and bis-[ $\beta$ -(4-azidosalicylamido)ethyl]disulfide (BASED) and N-succinimidyl-6(4'-azido-2'-nitrophenyl-amino)hexanoate (SANPAH) are examples of useful photoreactive cross-linkers for use in this invention. For a recent review of protein coupling techniques, see Means et al. (1990) *Bioconjugate Chemistry* 1:2-12, incorporated by reference herein.

One particularly useful class of heterobifunctional cross-linkers, included above, contain the primary amine reactive group, N-hydroxysuccinimide (NHS), or its water soluble analog N-hydroxysulfosuccinimide (sulfo-NHS). Primary amines (lysine epsilon groups) at alkaline pH's are unprotonated and react by nucleophilic attack on NHS or sulfo-NHS esters. This reaction results in the formation of an amide bond, and release of NHS or sulfo-NHS as a by-product.

Another reactive group useful as part of a heterobifunctional cross-linker is a thiol reactive group. Common thiol reactive groups include maleimides, halogens, and pyridyl disulfides. Maleimides react specifically with free sulfhydryls (cysteine residues) in minutes, under slightly acidic to neutral (pH 6.5-7.5) conditions. Halogens (iodoacetyl functions) react with -SH groups at physiological pH's. Both of these reactive groups result in the formation of stable thioether bonds.

The third component of the heterobifunctional cross-linker is the spacer arm or bridge. The bridge is the structure that connects the two reactive ends. The most apparent attribute of the bridge is its effect on steric hindrance. In some instances, a longer bridge can more easily span the distance necessary to link two complex biomolecules. For instance, SMPB has a span of 14.5 angstroms.

Preparing protein-protein conjugates using heterobifunctional reagents is a two-step process involving the amine reaction and the sulfhydryl reaction. For the first step, the amine reaction, the protein chosen should contain a primary amine. This can be lysine epsilon amines or a primary alpha amine found at the N-terminus of most proteins. The protein

should not contain free sulfhydryl groups. In cases where both proteins to be conjugated contain free sulfhydryl groups, one protein can be modified so that all sulfhydryls are blocked using for instance, N-ethylmaleimide (see Partis et al. (1983) J. Pro. Chem. 2:263, incorporated by reference herein). Ellman's Reagent can be used to calculate the quantity of  
5 sulfhydryls in a particular protein (see for example Ellman et al. (1958) Arch. Biochem. Biophys. 74:443 and Riddles et al. (1979) Anal. Biochem. 94:75, incorporated by reference herein).

The reaction buffer should be free of extraneous amines and sulfhydryls. The pH of the reaction buffer should be 7.0-7.5. This pH range prevents maleimide groups from  
10 reacting with amines, preserving the maleimide group for the second reaction with sulfhydryls.

The NHS-ester containing cross-linkers have limited water solubility. They should be dissolved in a minimal amount of organic solvent (DMF or DMSO) before introducing the cross-linker into the reaction mixture. The cross-linker/solvent forms an emulsion which will  
15 allow the reaction to occur.

The sulfo-NHS ester analogs are more water soluble, and can be added directly to the reaction buffer. Buffers of high ionic strength should be avoided, as they have a tendency to "salt out" the sulfo-NHS esters. To avoid loss of reactivity due to hydrolysis, the cross-linker is added to the reaction mixture immediately after dissolving the protein solution.

20 The reactions can be more efficient in concentrated protein solutions. The more alkaline the pH of the reaction mixture, the faster the rate of reaction. The rate of hydrolysis of the NHS and sulfo-NHS esters will also increase with increasing pH. Higher temperatures will increase the reaction rates for both hydrolysis and acylation.

Once the reaction is completed, the first protein is now activated, with a sulfhydryl  
25 reactive moiety. The activated protein may be isolated from the reaction mixture by simple gel filtration or dialysis. To carry out the second step of the cross-linking, the sulfhydryl reaction, the lipophilic group chosen for reaction with maleimides, activated halogens, or pyridyl disulfides must contain a free sulfhydryl. Alternatively, a primary amine may be modified with to add a sulfhydryl

30 In all cases, the buffer should be degassed to prevent oxidation of sulfhydryl groups. EDTA may be added to chelate any oxidizing metals that may be present in the buffer. Buffers should be free of any sulfhydryl containing compounds.

Maleimides react specifically with -SH groups at slightly acidic to neutral pH ranges (6.5-7.5). A neutral pH is sufficient for reactions involving halogens and pyridyl disulfides.  
35 Under these conditions, maleimides generally react with -SH groups within a matter of minutes. Longer reaction times are required for halogens and pyridyl disulfides.



The first sulfhydryl reactive-protein prepared in the amine reaction step is mixed with the sulfhydryl-containing lipophilic group under the appropriate buffer conditions. The conjugates can be isolated from the reaction mixture by methods such as gel filtration or by dialysis.

5 Exemplary activated lipophilic moieties for conjugation include: N-(1-pyrene)maleimide; 2,5-dimethoxystilbene-4'-maleimide, eosin-5-maleimide; fluorescein-5-maleimide; N-(4-(6-dimethylamino-2-benzofuranyl)phenyl)maleimide; benzophenone-4-maleimide; 4-dimethylaminophenylazophenyl-4'-maleimide (DABMI), tetramethylrhodamine-5-maleimide, tetramethylrhodamine-6-maleimide, Rhodamine Red<sup>TM</sup> C2 maleimide, N-(5-aminopentyl)maleimide, trifluoroacetic acid salt, N-(2-aminoethyl)maleimide, trifluoroacetic acid salt, Oregon Green<sup>TM</sup> 488 maleimide, N-(2-(((4-azido-2,3,5,6-tetrafluoro)benzoyl)amino)ethyl)dithio)ethyl)maleimide (TFPAM-SS1), 2-(1-(3-dimethylaminopropyl)-indol-3-yl)-3-(indol-3-yl) maleimide (bisindolylmaleimide; GF 109203X), BODIPY<sup>®</sup> FL N-(2-aminoethyl)maleimide, N-(7-dimethylamino-4-methylcoumarin-3-yl)maleimide (DACM), Alexa<sup>TM</sup> 488 C5 maleimide, Alexa<sup>TM</sup> 594 C5 maleimide, sodium salt N-(1-pyrene)maleimide, 2,5-dimethoxystilbene-4'-maleimide, eosin-5-maleimide, fluorescein-5-maleimide, N-(4-(6-dimethylamino-2-benzofuranyl)phenyl)maleimide, benzophenone-4-maleimide, 4-dimethylaminophenylazophenyl-4'-maleimide, 1-(2-maleimidylethyl)-4-(5-(4-methoxyphenyl)oxazol-2-yl)pyridinium methanesulfonate, tetramethylrhodamine-5-maleimide, tetramethylrhodamine-6-maleimide, Rhodamine Red<sup>TM</sup> C2 maleimide, N-(5-aminopentyl)maleimide, N-(2-aminoethyl)maleimide, N-(2-(((4-azido-2,3,5,6-tetrafluoro)benzoyl)amino)ethyl)dithio)ethyl)maleimide, 2-(1-(3-dimethylaminopropyl)-indol-3-yl)-3-(indol-3-yl) maleimide, N-(7-dimethylamino-4-methylcoumarin-3-yl)maleimide (DACM), 11H-Benzo[a]fluorene, Benzo[a]pyrene.

In one embodiment, the *hedgehog* polypeptide can be derivatized using pyrene maleimide, which can be purchased from Molecular Probes (Eugene, Oreg.), e.g., N-(1-pyrene)maleimide or 1-pyrenemethyl iodoacetate (PMIA ester). As illustrated in Figure 1, the pyrene-derived *hedgehog* polypeptide had an activity profile indicating that it was nearly 2 orders of magnitude more active than the unmodified form of the protein.

For those embodiments wherein the hydrophobic moiety is a polypeptide, the modified *hedgehog* polypeptide of this invention can be constructed as a fusion protein, containing the *hedgehog* polypeptide and the hydrophobic moiety as one contiguous polypeptide chain.

In certain embodiments, the lipophilic moiety is an amphipathic polypeptide, such as magainin, cecropin, attacin, melittin, gramicidin S, alpha-toxin of *Staph. aureus*, alamethicin or a synthetic amphipathic polypeptide. Fusogenic coat proteins from viral particles can also be a convenient source of amphipathic sequences for the subject *hedgehog* polypeptides

Moreover, mutagenesis can be used to create modified *hh* polypeptides, e.g., for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*). Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. Modified *hedgehog* polypeptides can also include those with altered post-translational processing relative to a naturally occurring *hedgehog* polypeptide, e.g., altered glycosylation, cholesterolization, prenylation and the like.

In one embodiment, the *hedgehog* therapeutic is a polypeptide encodable by a nucleotide sequence that hybridizes under stringent conditions to a *hedgehog* coding sequence represented in one or more of SEQ ID Nos:1-9 or 19. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C.

As described in the literature, genes for other *hedgehog* polypeptides, e.g., from other animals, can be obtained from mRNA or genomic DNA samples using techniques well known in the art. For example, a cDNA encoding a *hedgehog* polypeptide can be obtained by isolating total mRNA from a cell, e.g. a mammalian cell, e.g. a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene encoding a *hedgehog* polypeptide can also be cloned using established polymerase chain reaction techniques.

Preferred nucleic acids encode a *hedgehog* polypeptide comprising an amino acid sequence at least 60% homologous, more preferably 70% homologous and most preferably 80% homologous with an amino acid sequence selected from the group consisting of SEQ ID Nos:8-14. Nucleic acids which encode polypeptides at least about 90%, more preferably at least about 95%, and most preferably at least about 98-99% homology with an amino acid sequence represented in one of SEQ ID Nos:10-18 or 20 are also within the scope of the invention.

*Hedgehog* polypeptides preferred by the present invention, in addition to native *hedgehog* polypeptides, are at least 60% homologous, more preferably 70% homologous and most preferably 80% homologous with an amino acid sequence represented by any of SEQ ID Nos:10-18 or 20. Polypeptides which are at least 90%, more preferably at least 95%, and

most preferably at least about 98-99% homologous with a sequence selected from the group consisting of SEQ ID Nos:10-18 or 20 are also within the scope of the invention. The only prerequisite is that the *hedgehog* polypeptide is capable of protecting neuronal cells against degeneration, e.g., the polypeptide is trophic for a dopaminergic and/or GABAergic neuron.

5           The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a *hedgehog* polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant *hedgehog* gene, is meant to include within the meaning of  
10 "recombinant protein" those proteins having an amino acid sequence of a native *hedgehog* polypeptide, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the protein.

          The method of the present invention can also be carried out using variant forms of the  
15 naturally occurring *hedgehog* polypeptides, e.g., mutational variants.

          As is known in the art, *hedgehog* polypeptides can be produced by standard biological techniques. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. The polypeptide *hedgehog*  
20 may be secreted and isolated from a mixture of cells and medium containing the recombinant *hedgehog* polypeptide. Alternatively, the peptide may be retained cytoplasmically by removing the signal peptide sequence from the recombinant *hedgehog* gene and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well known in the art. The recombinant  
25 *hedgehog* polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred embodiment, the recombinant *hedgehog* polypeptide is a fusion protein containing a domain which facilitates its  
30 purification, such as an *hedgehog*/GST fusion protein. The host cell may be any prokaryotic or eukaryotic cell.

          Recombinant *hedgehog* genes can be produced by ligating nucleic acid encoding an *hedgehog* polypeptide, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells, or both. Expression vectors for production of recombinant  
35 forms of the subject *hedgehog* polypeptides include plasmids and other vectors. For instance, suitable vectors for the expression of a *hedgehog* polypeptide include plasmids of the types:

pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach *et al.* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein). These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, an *hedgehog* polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning the coding sequence of one of the *hedgehog* genes represented in SEQ ID Nos:1-9 or 19.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNA1/amp, pcDNA1/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHyg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papillomavirus (BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205) can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

In some instances, it may be desirable to express the recombinant *hedgehog* polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the  $\beta$ -gal containing pBlueBac III).

When it is desirable to express only a portion of a *hedgehog* polypeptide, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine

aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat et al. (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller et al. (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing  
5 *hedgehog*-derived polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller et al., *supra*).

Alternatively, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. It is widely appreciated that fusion proteins can also facilitate the expression of proteins, and  
10 accordingly, can be used in the expression of the *hedgehog* polypeptides of the present invention. For example, *hedgehog* polypeptides can be generated as glutathione-S-transferase (GST-fusion) proteins. Such GST-fusion proteins can enable easy purification of the *hedgehog* polypeptide, as for example by the use of glutathione-derivatized matrices (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. (N.Y.: John Wiley &  
15 Sons, 1991)). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence, can be used to replace the signal sequence which naturally occurs at the N-terminus of the *hedgehog* polypeptide (e.g. of the pro-form, in order to permit purification of the poly(His)-*hedgehog* polypeptide by affinity chromatography using a Ni<sup>2+</sup> metal resin. The purification leader sequence can then be  
20 subsequently removed by treatment with enterokinase (e.g., see Hochuli et al. (1987) *J. Chromatography* 411:177; and Janknecht et al. *PNAS* 88:8972).

Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-  
25 ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to  
30 complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992).

*Hedgehog* polypeptides may also be chemically modified to create *hedgehog* derivatives by forming covalent or aggregate conjugates with other chemical moieties, such  
35 as glycosyl groups, cholesterol, isoprenoids, lipids, phosphate, acetyl groups and the like. Covalent derivatives of *hedgehog* polypeptides can be prepared by linking the chemical

moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

For instance, *hedgehog* polypeptides can be generated to include a moiety, other than sequence naturally associated with the protein, that binds a component of the extracellular matrix and enhances localization of the analog to cell surfaces. For example, sequences derived from the fibronectin "type-III repeat", such as a tetrapeptide sequence R-G-D-S (Pierschbacher et al. (1984) *Nature* 309:30-3; and Kornblihtt et al. (1985) *EMBO* 4:1755-9) can be added to the *hedgehog* polypeptide to support attachment of the chimeric molecule to a cell through binding ECM components (Ruoslahti et al. (1987) *Science* 238:491-497; Pierschbacher et al. (1987) *J. Biol. Chem.* 262:17294-8.; Hynes (1987) *Cell* 48:549-54; and Hynes (1992) *Cell* 69:11-25).

In preferred embodiment, the *hedgehog* polypeptide is isolated from, or is otherwise substantially free of, other cellular proteins, especially other extracellular or cell surface associated proteins which may normally be associated with the *hedgehog* polypeptide. The term "substantially free of other cellular or extracellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of *hedgehog* polypeptides having less than 20% (by dry weight) contaminating protein, and preferably having less than 5% contaminating protein. By "purified", it is meant that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins. The term "purified" as used herein preferably means at least 80% by dry weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above.

As described above for recombinant polypeptides, isolated *hedgehog* polypeptides can include all or a portion of the amino acid sequences represented in any of SEQ ID Nos:10-18 or 20, or a homologous sequence thereto. Preferred fragments of the subject *hedgehog* polypeptides correspond to the N-terminal and C-terminal proteolytic fragments of the mature protein. Bioactive fragments of *hedgehog* polypeptides are described in great detail in PCT publications WO 95/18856 and WO 96/17924.

With respect to bioactive fragments of *hedgehog* polypeptide, preferred *hedgehog* therapeutics include at least 50 amino acid residues of a *hedgehog* polypeptide, more preferably at least 100, and even more preferably at least 150.

Another preferred *hedgehog* polypeptide which can be included in the *hedgehog* therapeutic is an N-terminal fragment of the mature protein having a molecular weight of approximately 19 kDa.

Preferred human *hedgehog* polypeptides include N-terminal fragments corresponding  
 5 approximately to residues 24-197 of SEQ ID No. 15, 28-202 of SEQ ID No. 16, and 23-198 of SEQ ID No. 17. By "corresponding approximately" it is meant that the sequence of interest is at most 20 amino acid residues different in length to the reference sequence, though more preferably at most 5, 10 or 15 amino acid different in length.

Still other preferred *hedgehog* polypeptides includes an amino acid sequence  
 10 represented by the formula A-B wherein: (i) A represents all or the portion of the amino acid sequence designated by residues 1-168 of SEQ ID No:21; and B represents at least one amino acid residue of the amino acid sequence designated by residues 169-221 of SEQ ID No:21; (ii) A represents all or the portion of the amino acid sequence designated by residues 24-193 of SEQ ID No:15; and B represents at least one amino acid residue of the amino acid  
 15 sequence designated by residues 194-250 of SEQ ID No:15; (iii) A represents all or the portion of the amino acid sequence designated by residues 25-193 of SEQ ID No:13; and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of SEQ ID No:13; (iv) A represents all or the portion of the amino acid sequence designated by residues 23-193 of SEQ ID No:11; and B represents at least one amino acid  
 20 residue of the amino acid sequence designated by residues 194-250 of SEQ ID No:11; (v) A represents all or the portion of the amino acid sequence designated by residues 28-197 of SEQ ID No:12; and B represents at least one amino acid residue of the amino acid sequence designated by residues 198-250 of SEQ ID No:12; (vi) A represents all or the portion of the amino acid sequence designated by residues 29-197 of SEQ ID No:16; and B represents at  
 25 least one amino acid residue of the amino acid sequence designated by residues 198-250 of SEQ ID No:16; or (vii) A represents all or the portion of the amino acid sequence designated by residues 23-193 of SEQ ID No. 17, and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of SEQ ID No. 17. In certain preferred embodiments, A and B together represent a contiguous polypeptide sequence designated  
 30 sequence, A represents at least 25, 50, 75, 100, 125 or 150 amino acids of the designated sequence, and B represents at least 5, 10, or 20 amino acid residues of the amino acid sequence designated by corresponding entry in the sequence listing, and A and B together preferably represent a contiguous sequence corresponding to the sequence listing entry. Similar fragments from other *hedgehog* also contemplated, e.g., fragments which correspond  
 35 to the preferred fragments from the sequence listing entries which are enumerated above.

Isolated peptidyl portions of *hedgehog* polypeptides can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid

encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a *hedgehog* polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably  
5 divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as agonists of a wild-type (e.g., "authentic") *hedgehog* polypeptide. For example, Román et al. (1994) *Eur J Biochem* 222:65-73 describe the use of competitive-binding assays using short, overlapping synthetic peptides from larger proteins to identify  
10 binding domains.

The recombinant *hedgehog* polypeptides of the present invention also include homologs of the authentic *hedgehog* polypeptides, such as versions of those protein which are resistant to proteolytic cleavage, as for example, due to mutations which alter potential cleavage sequences or which inactivate an enzymatic activity associated with the protein.  
15 *Hedgehog* homologs of the present invention also include proteins which have been post-translationally modified in a manner different than the authentic protein. Exemplary derivatives of *hedgehog* polypeptides include polypeptides which lack glycosylation sites (e.g. to produce an unglycosylated protein), which lack sites for cholesterolization, and/or which lack N-terminal and/or C-terminal sequences.

20 Modification of the structure of the subject *hedgehog* polypeptides can also be for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein, are considered functional equivalents of the *hedgehog* polypeptides described in more detail  
25 herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition.

It is well known in the art that certain isolated replacements of amino acids, e.g., replacement of an amino acid residue with another related amino acid (i.e. isosteric and/or isoelectric mutations), can be carried out without major effect on the biological activity of the  
30 resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids are can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine,  
35 serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic =



glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur -containing = cysteine and methionine. (see, for example, *Biochemistry*, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional *hedgehog* homolog (e.g. functional in the sense that it acts to mimic or antagonize the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response. Polypeptides in which more than one replacement has taken place can readily be tested in the same manner.

It is specifically contemplated that the methods of the present invention can be carried using homologs of naturally occurring *hedgehog* polypeptides. In one embodiment, the invention contemplates using *hedgehog* polypeptides generated by combinatorial mutagenesis. Such methods, as are known in the art, are convenient for generating both point and truncation mutants, and can be especially useful for identifying potential variant sequences (e.g. homologs) that are functional in binding to a receptor for *hedgehog* polypeptides. The purpose of screening such combinatorial libraries is to generate, for example, novel *hedgehog* homologs which can act as neuroprotective agents. To illustrate, *hedgehog* homologs can be engineered by the present method to provide more efficient binding to a cognate receptor, such as *patched*, retaining neuroprotective activity. Thus, combinatorially-derived homologs can be generated to have an increased potency relative to a naturally occurring form of the protein. Moreover, manipulation of certain domains of *hedgehog* by the present method can provide domains more suitable for use in fusion proteins, such as one that incorporates portions of other proteins which are derived from the extracellular matrix and/or which bind extracellular matrix components.

To further illustrate the state of the art of combinatorial mutagenesis, it is noted that the review article of Gallop et al. (1994) *J Med Chem* 37:1233 describes the general state of the art of combinatorial libraries as of the earlier 1990's. In particular, Gallop et al state at page 1239 "[s]creening the analog libraries aids in determining the minimum size of the active sequence and in identifying those residues critical for binding and intolerant of substitution". In addition, the Ladner et al. PCT publication WO90/02809, the Goeddel et al. U.S. Patent 5,223,408, and the Markland et al. PCT publication WO92/15679 illustrate specific techniques which one skilled in the art could utilize to generate libraries of *hedgehog* variants which can be rapidly screened to identify variants/fragments which retained a particular activity of the *hedgehog* polypeptides. These techniques are exemplary of the art and demonstrate that large libraries of related variants/truncants can be generated and assayed to isolate particular variants without undue experimentation. Gustin et al. (1993) *Virology*

193:653, and Bass et al. (1990) *Proteins: Structure, Function and Genetics* 8:309-314

also describe other exemplary techniques from the art which can be adapted as means for generating mutagenic variants of *hedgehog* polypeptides.

Indeed, it is plain from the combinatorial mutagenesis art that large scale mutagenesis of *hedgehog* polypeptides, without any preconceived ideas of which residues were critical to the biological function, and generate wide arrays of variants having equivalent biological activity. Indeed, it is the ability of combinatorial techniques to screen billions of different variants by high throughput analysis that removes any requirement of *a priori* understanding or knowledge of critical residues.

To illustrate, the amino acid sequences for a population of *hedgehog* homologs or other related proteins are aligned, preferably to promote the highest homology possible. Such a population of variants can include, for example, *hedgehog* homologs from one or more species. Amino acids which appear at each position of the aligned sequences are selected to create a degenerate set of combinatorial sequences. In a preferred embodiment, the variegated library of *hedgehog* variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For instance, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential *hedgehog* sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display) containing the set of *hedgehog* sequences therein.

As illustrated in PCT publication WO 95/18856, to analyze the sequences of a population of variants, the amino acid sequences of interest can be aligned relative to sequence homology. The presence or absence of amino acids from an aligned sequence of a particular variant is relative to a chosen consensus length of a reference sequence, which can be real or artificial.

In an illustrative embodiment, alignment of exons 1, 2 and a portion of exon 3 encoded sequences (e.g. the N-terminal approximately 221 residues of the mature protein) of each of the *Shh* clones produces a degenerate set of *Shh* polypeptides represented by the general formula:

C-G-P-G-R-G-X(1)-G-X(2)-R-R-H-P-K-K-L-T-P-L-A-Y-K-Q-F-I-P-N-V-A-  
E-K-T-L-G-A-S-G-R-Y-E-G-K-I-X(3)-R-N-S-E-R-F-K-E-L-T-P-N-Y-N-P-D-  
I-I-F-K-D-E-E-N-T-G-A-D-R-L-M-T-Q-R-C-K-D-K-L-N-X(4)-L-A-I-S-V-  
M-N-X(5)-W-P-G-V-X(6)-L-R-V-T-E-G-W-D-E-D-G-H-H-X(7)-E-E-S-L-H-  
Y-E-G-R-A-V-D-I-T-T-S-D-R-D-X(8)-S-K-Y-G-X(9)-L-X(10)-R-L-A-V-E-  
A-G-F-D-W-V-Y-Y-E-S-K-A-H-I-H-C-S-V-K-A-E-N-S-V-A-A-K-S-G-G-C-  
F-P-G-S-A-X(11)-V-X(12)-L-X(13)-X(14)-G-G-X(15)-K-X(16)-V-K-D-L-

X(17)-P-G-D-X(18)-V-L-A-A-D-X(19)-X(20)-G-X(21)-L-X(22)-X(23)-S-D-  
F-X(24)-X(25)-F-X(26)-D-R (SEQ ID No: 21),

wherein each of the degenerate positions "X" can be an amino acid which occurs in that position in one of the human, mouse, chicken or zebrafish *Shh* clones, or, to expand the library, each X can also be selected from amongst amino acid residue which would be conservative substitutions for the amino acids which appear naturally in each of those positions. For instance, Xaa(1) represents Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp ; Xaa(2) represents Arg, His or Lys; Xaa(3) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(4) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(5) represents Lys, Arg, His, Asn or Gln; Xaa(6) represents Lys, Arg or His; Xaa(7) represents Ser, Thr, Tyr, Trp or Phe; Xaa(8) represents Lys, Arg or His; Xaa(9) represents Met, Cys, Ser or Thr; Xaa(10) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(11) represents Leu, Val, Met, Thr or Ser; Xaa(12) represents His, Phe, Tyr, Ser, Thr, Met or Cys; Xaa(13) represents Gln, Asn, Glu, or Asp; Xaa(14) represents His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp; Xaa(15) represents Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys; Xaa(16) represents Ala, Gly, Cys, Leu, Val or Met; Xaa(17) represents Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys; Xaa(18) represents Arg, Lys, Met or Ile; Xaa(19) represents Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met; Xaa(20) represents Ala, Gly, Cys, Asp, Asn, Glu or Gln; Xaa(21) represents Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln; Xaa(22) represent Leu, Val, Met or Ile; Xaa(23) represents Phe, Tyr, Thr, His or Trp; Xaa(24) represents Ile, Val, Leu or Met; Xaa(25) represents Met, Cys, Ile, Leu, Val, Thr or Ser; Xaa(26) represents Leu, Val, Met, Thr or Ser. In an even more expansive library, each X can be selected from any amino acid.

In similar fashion, alignment of each of the human, mouse, chicken and zebrafish *hedgehog* clones, can provide a degenerate polypeptide sequence represented by the general formula:

C-G-P-G-R-G-X(1)-X(2)-X(3)-R-R-X(4)-X(5)-X(6)-P-K-X(7)-L-X(8)-P-L-  
X(9)-Y-K-Q-F-X(10)-P-X(11)-X(12)-X(13)-E-X(14)-T-L-G-A-S-G-X(15)-  
X(16)-E-G-X(17)-X(18)-X(19)-R-X(20)-S-E-R-F-X(21)-X(22)-L-T-P-N-Y-  
N-P-D-I-I-F-K-D-E-E-N-X(23)-G-A-D-R-L-M-T-X(24)-R-C-K-X(25)-X(26)-  
X(27)-N-X(28)-L-A-I-S-V-M-N-X(29)-W-P-G-V-X(30)-L-R-V-T-E-G-  
X(31)-D-E-D-G-H-H-X(32)-X(33)-X(34)-S-L-H-Y-E-G-R-A-X(35)-D-I-T-T-  
S-D-R-D-X(36)-X(37)-K-Y-G-X(38)-L-X(39)-R-L-A-V-E-A-G-F-D-W-V-Y-  
Y-E-S-X(40)-X(41)-H-X(42)-H-X(43)-S-V-K-X(44)-X(45) (SEQIDNo:22),

wherein, as above, each of the degenerate positions "X" can be an amino acid which occurs in a corresponding position in one of the wild-type clones, and may also include amino acid residue which would be conservative substitutions, or each X can be any amino acid residue. In an exemplary embodiment, Xaa(1) represents Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr;

Xaa(2) represents Gly, Ala, Val, Leu or Ile; Xaa(3) represents Gly, Ala, Val, Leu, Ile, Lys, His or Arg; Xaa(4) represents Lys, Arg or His; Xaa(5) represents Phe, Trp, Tyr or an amino acid gap; Xaa(6) represents Gly, Ala, Val, Leu, Ile or an amino acid gap; Xaa(7) represents Asn, Gln, His, Arg or Lys; Xaa(8) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(9) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(10) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(11) represents Ser, Thr, Gln or Asn; Xaa(12) represents Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(13) represents Gly, Ala, Val, Leu, Ile or Pro; Xaa(14) represents Arg, His or Lys; Xaa(15) represents Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys; Xaa(16) represents Gly, Ala, Val, Leu, Ile, Phe or Tyr; Xaa(17) represents Arg, His or Lys; Xaa(18) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(19) represents Thr or Ser; Xaa(20) represents Gly, Ala, Val, Leu, Ile, Asn or Gln; Xaa(21) represents Arg, His or Lys; Xaa(22) represents Asp or Glu; Xaa(23) represents Ser or Thr; Xaa(24) represents Glu, Asp, Gln or Asn; Xaa(25) represents Glu or Asp; Xaa(26) represents Arg, His or Lys; Xaa(27) represents Gly, Ala, Val, Leu or Ile; Xaa(28) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; Xaa(29) represents Met, Cys, Gln, Asn, Arg, Lys or His; Xaa(30) represents Arg, His or Lys; Xaa(31) represents Trp, Phe, Tyr, Arg, His or Lys; Xaa(32) represents Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe; Xaa(33) represents Gln, Asn, Asp or Glu; Xaa(34) represents Asp or Glu; Xaa(35) represents Gly, Ala, Val, Leu, or Ile; Xaa(36) represents Arg, His or Lys; Xaa(37) represents Asn, Gln, Thr or Ser; Xaa(38) represents Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys; Xaa(39) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; Xaa(40) represents Arg, His or Lys; Xaa(41) represents Asn, Gln, Gly, Ala, Val, Leu or Ile; Xaa(42) represents Gly, Ala, Val, Leu or Ile; Xaa(43) represents Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys; Xaa(44) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; and Xaa(45) represents Asp or Glu.

There are many ways by which the library of potential *hedgehog* homologs can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential *hedgehog* sequences. The synthesis of degenerate oligonucleotides is well known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249:404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of *hedgehog* homologs. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as necessary to screen large numbers of degenerate *hedgehog* sequences created by combinatorial mutagenesis techniques.

In one embodiment, the combinatorial library is designed to be secreted (e.g. the polypeptides of the library all include a signal sequence but no transmembrane or cytoplasmic domains), and is used to transfect a eukaryotic cell that can be co-cultured with neuronal cells. A functional *hedgehog* polypeptide secreted by the cells expressing the combinatorial library will diffuse to neighboring neuronal cells and induce a particular biological response, such as protection against cell death when treated with MPTP. The pattern of protection will resemble a gradient function, and will allow the isolation (generally after several repetitive rounds of selection) of cells producing *hedgehog* homologs active as neuroprotective agents with respect to the target neuronal cells

To illustrate, target neuronal cells are cultured in 24-well microtitre plates. Other eukaryotic cells are transfected with the combinatorial *hedgehog* gene library and cultured in cell culture inserts (e.g. Collaborative Biomedical Products, Catalog #40446) that are able to fit into the wells of the microtitre plate. The cell culture inserts are placed in the wells such that recombinant *hedgehog* homologs secreted by the cells in the insert can diffuse through the porous bottom of the insert and contact the target cells in the microtitre plate wells. After a period of time sufficient for functional forms of a *hedgehog* polypeptide to produce a measurable response in the target cells, such as neuroprotection, the inserts are removed and the effect of the variant *hedgehog* polypeptides on the target cells determined. Cells from the inserts corresponding to wells which score positive for activity can be split and re-cultured on several inserts, the process being repeated until the active clones are identified.

In yet another screening assay, the candidate *hedgehog* gene products are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to associate with a *hedgehog*-binding moiety (such as the *patched* protein or other *hedgehog* receptor) via this gene product is detected in a "panning assay". Such panning steps can be carried out on cells cultured from embryos. For instance, the gene library can be cloned into

the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, fluorescently labeled molecules which bind *hedgehog* can be used to score for potentially functional  
5 *hedgehog* homologs. Cells can be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, separated by a fluorescence-activated cell sorter.

In an alternate embodiment, the gene library is expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide  
10 sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at very high concentrations, large number of phage can be screened at one time. Second, since each infectious phage displays the combinatorial gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round  
15 of infection. The group of almost identical *E.coli* filamentous phages M13, fd, and f1 are most often used in phage display libraries, as either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO*  
20 *J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

In an illustrative embodiment, the recombinant phage antibody system (RPAS, Pharmacia Catalog number 27-9400-01) can be easily modified for use in expressing and screening *hedgehog* combinatorial libraries. For instance, the pCANTAB 5 phagemid of the  
25 RPAS kit contains the gene which encodes the phage gIII coat protein. The *hedgehog* combinatorial gene library can be cloned into the phagemid adjacent to the gIII signal sequence such that it will be expressed as a gIII fusion protein. After ligation, the phagemid is used to transform competent *E. coli* TG1 cells. Transformed cells are subsequently infected with M13KO7 helper phage to rescue the phagemid and its candidate *hedgehog* gene insert.  
30 The resulting recombinant phage contain phagemid DNA encoding a specific candidate *hedgehog*, and display one or more copies of the corresponding fusion coat protein. The phage-displayed candidate *hedgehog* polypeptides which are capable of binding an *hedgehog* receptor are selected or enriched by panning. For instance, the phage library can be applied to cells which express the *patched* protein and unbound phage washed away from the cells. The  
35 bound phage is then isolated, and if the recombinant phage express at least one copy of the wild type gIII coat protein, they will retain their ability to infect *E. coli*. Thus, successive rounds of reinfection of *E. coli*, and panning will greatly enrich for *hedgehog* homologs,

which can then be screened for further biological activities in order to differentiate agonists and antagonists.

Combinatorial mutagenesis has a potential to generate very large libraries of mutant proteins, e.g., in the order of  $10^{26}$  molecules. Combinatorial libraries of this size may be technically challenging to screen even with high throughput screening assays such as phage display. To overcome this problem, a new technique has been developed recently, recursive ensemble mutagenesis (REM), which allows one to avoid the very high proportion of non-functional proteins in a random library and simply enhances the frequency of functional proteins, thus decreasing the complexity required to achieve a useful sampling of sequence space. REM is an algorithm which enhances the frequency of functional mutants in a library when an appropriate selection or screening method is employed (Arkin and Yourvan, 1992, *PNAS USA* 89:7811-7815; Yourvan et al., 1992, *Parallel Problem Solving from Nature*, 2., In Maenner and Manderick, eds., Elsevir Publishing Co., Amsterdam, pp. 401-410; Delgrave et al., 1993, *Protein Engineering* 6(3):327-331).

The invention also provides for reduction of the *hedgehog* polypeptide to generate mimetics, e.g. peptide or non-peptide agents, which are able to mimic the neuroprotective activity of a naturally-occurring *hedgehog* polypeptide. Thus, such mutagenic techniques as described above are also useful to map the determinants of the *hedgehog* polypeptides which participate in protein-protein interactions involved in, for example, binding of the subject *hedgehog* polypeptide to other extracellular matrix components such as its receptor(s). To illustrate, the critical residues of a subject *hedgehog* polypeptide which are involved in molecular recognition of an *hedgehog* receptor such as *patched* can be determined and used to generate *hedgehog*-derived peptidomimetics which competitively bind with that moiety. By employing, for example, scanning mutagenesis to map the amino acid residues of each of the subject *hedgehog* polypeptides which are involved in binding other extracellular proteins, peptidomimetic compounds can be generated which mimic those residues of the *hedgehog* polypeptide which facilitate the interaction. After distinguishing between agonist and antagonists, such agonistic mimetics may be used to mimic the normal function of a *hedgehog* polypeptide as trophic for dopaminergic and GABAergic neurons. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co.

Rockland, IL, 1985),  $\beta$ -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and  $\beta$ -aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

5           Recombinantly produced forms of the *hedgehog* polypeptides can be produced using, e.g., expression vectors containing a nucleic acid encoding a *hedgehog* polypeptide, operably linked to at least one transcriptional regulatory sequence. Operably linked is intended to mean that the nucleotide sequence is linked to a regulatory sequence in a manner which allows expression of the nucleotide sequence. Regulatory sequences are art-recognized and  
10       are selected to direct expression of a *hedgehog* polypeptide. Accordingly, the term transcriptional regulatory sequence includes promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). For instance, any of a wide variety of expression control sequences, sequences that control the  
15       expression of a DNA sequence when operatively linked to it, may be used in these vectors to express DNA sequences encoding *hedgehog* polypeptide. Such useful expression control sequences, include, for example, a viral LTR, such as the LTR of the Moloney murine leukemia virus, the early and late promoters of SV40, adenovirus or cytomegalovirus immediate early promoter, the lac system, the trp system, the TAC or TRC system, T7  
20       promoter whose expression is directed by T7 RNA polymerase, the major operator and promoter regions of phage  $\lambda$ , the control regions for fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, e.g., Pho5, the promoters of the yeast  $\alpha$ -mating factors, the polyhedron promoter of the baculovirus system and other sequences known to control the expression of genes of  
25       prokaryotic or eukaryotic cells or their viruses, and various combinations thereof. It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transformed and/or the type of protein desired to be expressed. Moreover, the vector's copy number, the ability to control that copy number and the expression of any other proteins encoded by the vector, such as antibiotic markers, should  
30       also be considered.

          In addition to providing a ready source of *hedgehog* polypeptides for purification, the gene constructs of the present invention can also be used as a part of a gene therapy protocol to deliver nucleic acids encoding a neuroprotective form of a *hedgehog* polypeptide. Thus, another aspect of the invention features expression vectors for *in vivo* transfection of a  
35       *hedgehog* polypeptide in particular cell types so as cause ectopic expression of a *hedgehog* polypeptide in neuronal tissue.



Formulations of such expression constructs may be administered in any biologically effective carrier, e.g. any formulation or composition capable of effectively delivering the recombinant gene to cells *in vivo*. Approaches include insertion of the *hedgehog* coding sequence in viral vectors including recombinant retroviruses, adenovirus, adeno-associated virus, and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. Viral vectors transfect cells directly; plasmid DNA can be delivered with the help of, for example, cationic liposomes (lipofectin) or derivatized (e.g. antibody conjugated), polylysine conjugates, gramicidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or CaPO<sub>4</sub> precipitation carried out *in vivo*. It will be appreciated that because transduction of appropriate target cells represents the critical first step in gene therapy, choice of the particular gene delivery system will depend on such factors as the phenotype of the intended target and the route of administration, e.g. locally or systemically. Furthermore, it will be recognized that the particular gene construct provided for *in vivo* transduction of *hedgehog* expression are also useful for *in vitro* transduction of cells, such as for use in the *ex vivo* tissue culture systems described below.

A preferred approach for *in vivo* introduction of nucleic acid into a cell is by use of a viral vector containing nucleic acid, e.g. a cDNA, encoding the particular form of the *hedgehog* polypeptide desired. Infection of cells with a viral vector has the advantage that a large proportion of the targeted cells can receive the nucleic acid. Additionally, molecules encoded within the viral vector, e.g., by a cDNA contained in the viral vector, are expressed efficiently in cells which have taken up viral vector nucleic acid.

Retrovirus vectors and adeno-associated virus vectors are generally understood to be the recombinant gene delivery system of choice for the transfer of exogenous genes *in vivo*, particularly into humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host. A major prerequisite for the use of retroviruses is to ensure the safety of their use, particularly with regard to the possibility of the spread of wild-type virus in the cell population. The development of specialized cell lines (termed "packaging cells") which produce only replication-defective retroviruses has increased the utility of retroviruses for gene therapy, and defective retroviruses are well characterized for use in gene transfer for gene therapy purposes (for a review see Miller, A.D. (1990) *Blood* 76:271). Thus, recombinant retrovirus can be constructed in which part of the retroviral coding sequence (*gag*, *pol*, *env*) has been replaced by nucleic acid encoding a *hedgehog* polypeptide and renders the retrovirus replication defective. The replication defective retrovirus is then packaged into virions which can be used to infect a target cell through the use of a helper virus by standard techniques. Protocols for producing recombinant retroviruses and for infecting cells *in vitro* or *in vivo* with such viruses can be found in Current Protocols in Molecular Biology, Ausubel, F.M. et

al. (eds.) Greene Publishing Associates, (1989), Sections 9.10-9.14 and other standard laboratory manuals. Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are well known to those skilled in the art. Examples of suitable packaging virus lines for preparing both ecotropic and amphotropic retroviral systems include Crip, Cre, 2 and Am.

5 Retroviruses have been used to introduce a variety of genes into many different cell types, including neuronal cells, *in vitro* and/or *in vivo* (see for example Eglitis, et al. (1985) *Science* 230:1395-1398; Danos and Mulligan (1988) *Proc. Natl. Acad. Sci. USA* 85:6460-6464; Wilson et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:3014-3018; Armentano et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6141-6145; Huber et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8039-

10 8043; Ferry et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8377-8381; Chowdhury et al. (1991) *Science* 254:1802-1805; van Beusechem et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:7640-7644; Kay et al. (1992) *Human Gene Therapy* 3:641-647; Dai et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:10892-10895; Hwu et al. (1993) *J. Immunol.* 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO

15 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573).

Furthermore, it has been shown that it is possible to limit the infection spectrum of retroviruses and consequently of retroviral-based vectors, by modifying the viral packaging proteins on the surface of the viral particle (see, for example PCT publications WO93/25234 and WO94/06920). For instance, strategies for the modification of the infection spectrum of

20 retroviral vectors include: coupling antibodies specific for cell surface antigens to the viral *env* protein (Roux et al. (1989) *PNAS* 86:9079-9083; Julan et al. (1992) *J. Gen Virol* 73:3251-3255; and Goud et al. (1983) *Virology* 163:251-254); or coupling cell surface receptor ligands to the viral *env* proteins (Neda et al. (1991) *J Biol Chem* 266:14143-14146). Coupling can be in the form of the chemical cross-linking with a protein or other variety (e.g.

25 lactose to convert the *env* protein to an asialoglycoprotein), as well as by generating fusion proteins (e.g. single-chain antibody/*env* fusion proteins). This technique, while useful to limit or otherwise direct the infection to certain tissue types, can also be used to convert an ecotropic vector in to an amphotropic vector.

Moreover, use of retroviral gene delivery can be further enhanced by the use of tissue-

30 or cell-specific transcriptional regulatory sequences which control expression of the *hedgehog* gene of the retroviral vector.

Another viral gene delivery system useful in the present method utilizes adenovirus-derived vectors. The genome of an adenovirus can be manipulated such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a

35 normal lytic viral life cycle. See for example Berkner et al. (1988) *BioTechniques* 6:616; Rosenfeld et al. (1991) *Science* 252:431-434; and Rosenfeld et al. (1992) *Cell* 68:143-155. Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other

strains of adenovirus (e.g., Ad2, Ad3, Ad7 etc.) are well known to those skilled in the art. Recombinant adenoviruses can be advantageous in certain circumstances in that they can be used to infect a wide variety of cell types, including neuronal cells (Rosenfeld et al. (1992) cited *supra*).

5           Furthermore, the virus particle is relatively stable and amenable to purification and concentration, and as above, can be modified so as to affect the spectrum of infectivity. Additionally, introduced adenoviral DNA (and foreign DNA contained therein) is not integrated into the genome of a host cell but remains episomal, thereby avoiding potential problems that can occur as a result of insertional mutagenesis in situations where introduced  
10       DNA becomes integrated into the host genome (e.g., retroviral DNA). Moreover, the carrying capacity of the adenoviral genome for foreign DNA is large (up to 8 kilobases) relative to other gene delivery vectors (Berkner et al. cited *supra*; Haj-Ahmand and Graham (1986) *J. Virol.* 57:267). Most replication-defective adenoviral vectors currently in use and therefore favored by the present invention are deleted for all or parts of the viral E1 and E3  
15       genes but retain as much as 80% of the adenoviral genetic material (see, e.g., Jones et al. (1979) *Cell* 16:683; Berkner et al., *supra*; and Graham et al. in Methods in Molecular Biology, E.J. Murray, Ed. (Humana, Clifton, NJ, 1991) vol. 7. pp. 109-127). Expression of the inserted *hedgehog* gene can be under control of, for example, the E1A promoter, the major late promoter (MLP) and associated leader sequences, the E3 promoter, or exogenously  
20       added promoter sequences.

          In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of a *hedgehog* polypeptide in the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred  
25       embodiments, non-viral gene delivery systems of the present invention rely on endocytic pathways for the uptake of the *hedgehog* polypeptide gene by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

          In clinical settings, the gene delivery systems for the therapeutic *hedgehog* gene can  
30       be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g. by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory  
35       sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced

by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 3054-3057). A *hedgehog* expression construct can be delivered in a gene therapy construct to dermal cells by, e.g., electroporation using techniques described, for example, by Dev et al. ((1994) *Cancer Treat Rev* 20:105-115).

5           The pharmaceutical preparation of the gene therapy construct can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery  
10           system.

          In yet another embodiment, the *hedgehog* or *ptc* therapeutic can be a "gene activation" construct which, by homologous recombination with a genomic DNA, alters the transcriptional regulatory sequences of an endogenous gene. For instance, the gene activation construct can replace the endogenous promoter of a *hedgehog* gene with a heterologous  
15           promoter, e.g., one which causes constitutive expression of the *hedgehog* gene or which causes inducible expression of the gene under conditions different from the normal expression pattern of the gene. Other genes in the *patched* signaling pathway can be similarly targeted. A variety of different formats for the gene activation constructs are available. See, for example, the Transkaryotic Therapies, Inc PCT publications WO93/09222, WO95/31560,  
20           WO96/29411, WO95/31560 and WO94/12650.

          In preferred embodiments, the nucleotide sequence used as the gene activation construct can be comprised of (1) DNA from some portion of the endogenous *hedgehog* gene (exon sequence, intron sequence, promoter sequences, etc.) which direct recombination and (2) heterologous transcriptional regulatory sequence(s) which is to be operably linked to the  
25           coding sequence for the genomic *hedgehog* gene upon recombination of the gene activation construct. For use in generating cultures of *hedgehog* producing cells, the construct may further include a reporter gene to detect the presence of the knockout construct in the cell.

          The gene activation construct is inserted into a cell, and integrates with the genomic DNA of the cell in such a position so as to provide the heterologous regulatory sequences in  
30           operative association with the native *hedgehog* gene. Such insertion occurs by homologous recombination, i.e., recombination regions of the activation construct that are homologous to the endogenous *hedgehog* gene sequence hybridize to the genomic DNA and recombine with the genomic sequences so that the construct is incorporated into the corresponding position of the genomic DNA.

35           The terms "recombination region" or "targeting sequence" refer to a segment (i.e., a portion) of a gene activation construct having a sequence that is substantially identical to or

substantially complementary to a genomic gene sequence, e.g., including 5' flanking sequences of the genomic gene, and can facilitate homologous recombination between the genomic sequence and the targeting transgene construct.

As used herein, the term "replacement region" refers to a portion of a activation  
5 construct which becomes integrated into an endogenous chromosomal location following homologous recombination between a recombination region and a genomic sequence.

The heterologous regulatory sequences, e.g., which are provided in the replacement  
10 region, can include one or more of a variety elements, including: promoters (such as constitutive or inducible promoters), enhancers, negative regulatory elements, locus control regions, transcription factor binding sites, or combinations thereof. Promoters/enhancers  
which may be used to control the expression of the targeted gene *in vivo* include, but are not limited to, the cytomegalovirus (CMV) promoter/enhancer (Karasuyama et al., 1989, *J. Exp. Med.*, 169:13), the human  $\beta$ -actin promoter (Gunning et al. (1987) *PNAS* 84:4831-4835), the glucocorticoid-inducible promoter present in the mouse mammary tumor virus long terminal  
15 repeat (MMTV LTR) (Klessig et al. (1984) *Mol. Cell Biol.* 4:1354-1362), the long terminal repeat sequences of Moloney murine leukemia virus (MuLV LTR) (Weiss et al. (1985) *RNA Tumor Viruses*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York), the SV40 early or late region promoter (Bernoist et al. (1981) *Nature* 290:304-310; Templeton et al. (1984) *Mol. Cell Biol.*, 4:817; and Sprague et al. (1983) *J. Virol.*, 45:773), the promoter  
20 contained in the 3' long terminal repeat of Rous sarcoma virus (RSV) (Yamamoto et al., 1980, *Cell*, 22:787-797), the herpes simplex virus (HSV) thymidine kinase promoter/enhancer (Wagner et al. (1981) *PNAS* 82:3567-71), and the herpes simplex virus LAT promoter (Wolfe et al. (1992) *Nature Genetics*, 1:379-384).

In an exemplary embodiment, portions of the 5' flanking region of the human Shh  
25 gene are amplified using primers which add restriction sites, to generate the following fragments

5' -gcgcgcttcgaaGCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCGGAGC-  
GAGGAAatcgatgcgcgc (primer 1)

30 5' -gcgcgcagatctGGGAAAGCGCAAGAGAGAGCGCACACGCACACACCCGCCGCGCG-  
CACTCGgatccgcgcgc (primer 2)

As illustrated, primer 1 includes a 5' non-coding region of the human Shh gene and is flanked  
by an *Asu*II and *Cla*I restriction sites. Primer 2 includes a portion of the 5' non-coding region  
35 immediately 3' to that present in primer 1. The *hedgehog* gene sequence is flanked by *Xho*II

and BamHI restriction sites. The purified amplimers are cut with each of the enzymes as appropriate.

The vector pCDNA1.1 (Invitrogen) includes a CMV promoter. The plasmid is cut with with AsuII, which cleaves just 3' to the CMV promoter sequence. The AsuII/ClaI fragment of primer 1 is ligated to the AsuII cleavage site of the pcDNA vector. The ClaI/AsuII ligation destroys the AsuII site at the 3' end of a properly inserted primer 1.

The vector is then cut with BamHI, and an XhoII/BamHI fragment of primer 2 is ligated to the BamHI cleavage site. As above, the BamHI/XhoII ligation destroys the BamHI site at the 5' end of a properly inserted primer 2.

Individual colonies are selected, cut with AsuII and BamHI, and the size of the AsuII/BamHI fragment determined. Colonies in which both the primer 1 and primer 2 sequences are correctly inserted are further amplified, an cut with AsuII and BamHI to produce the gene activation construct

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cgaagcgaggcagccagcgagggagagagcgagcgggagcgagccggagcgaggaaATCGAAGG
15  TTCGAATCCTTCCCCACCACCATCACTTTCAAAGTCCGAAAGAATCTGCTCCCTGCTTGT
   GTGTTGGAGGTGCTGAGTAGTGCGCGAGTAAATTTAAGCTACAACAAGGCAAGGCTTGAC
   CGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGG
   CCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCA
   TTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGG
20  CTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGC
   CAATAGGGACTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACTTGGCA
   GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCC
   CGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTTACTTGGCAGTACATCTACG
   TATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAG
25  CGGTTTGACTCACGGGGATTTCGAAGTCTCCACCCCATGACGTCAATGGGAGTTTGTTTTG
   GCACCAAATCAACGGGACTTTCCAAAATGTGCGTAACAACTCCGCCCCATTGACGCAAATGG
   GCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCC
   ACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTTGGTACCG
   AGCTCGGATCgatctgggaaagcgcaagagagagcgcacacgcacacacccgcccgcgcgcac
30  tcgg

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In this construct, the flanking primer 1 and primer 2 sequences provide the recombination region which permits the insertion of the CMV promoter in front of the coding sequence for the human *Shh* gene. Other heterologous promoters (or other transcriptional regulatory sequences) can be inserted in a genomic *hedgehog* gene by a similar method.

In still other embodiments, the replacement region merely deletes a negative transcriptional control element of the native gene, e.g., to activate expression, or ablates a positive control element, e.g., to inhibit expression of the targeted gene.

5    V. Exemplary *ptc* therapeutic compounds.

In another embodiment, the subject method is carried out using a *ptc* therapeutic composition. Such compositions can be generated with, for example, compounds which bind to patched and alter its signal transduction activity, compounds which alter the binding and/or enzymatic activity of a protein (e.g., intracellular) involved in patched signal pathway, and  
10    compounds which alter the level of expression of a *hedgehog* polypeptide, a patched protein or a protein involved in the intracellular signal transduction pathway of patched.

The availability of purified and recombinant *hedgehog* polypeptides facilitates the generation of assay systems which can be used to screen for drugs, such as small organic molecules, which are either agonists or antagonists of the normal cellular function of a  
15    *hedgehog* and/or patched protein, particularly in their role in the pathogenesis of neuronal cell death. In one embodiment, the assay evaluates the ability of a compound to modulate binding between a *hedgehog* polypeptide and a *hedgehog* receptor such as *patched*. In other embodiments, the assay merely scores for the ability of a test compound to alter the signal transduction activity of the *patched* protein. In this manner, a variety of *hedgehog* and/or *ptc*  
20    therapeutics, which will include ones with neuroprotective activity, can be identified. A variety of assay formats will suffice and, in light of the present disclosure, will be comprehended by skilled artisan.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds  
25    surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be  
30    generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with receptor proteins.

Accordingly, in an exemplary screening assay for *ptc* therapeutics, the compound of interest is contacted with a mixture including a *hedgehog* receptor protein (e.g., a cell  
35    expressing the *patched* receptor) and a *hedgehog* polypeptide under conditions in which it is ordinarily capable of binding the *hedgehog* polypeptide. To the mixture is then added a

composition containing a test compound. Detection and quantification of receptor/*hedgehog* complexes provides a means for determining the test compound's efficacy at inhibiting (or potentiating) complex formation between the receptor protein and the *hedgehog* polypeptide. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified *hedgehog* polypeptide is added to the receptor protein, and the formation of receptor/*hedgehog* complex is quantitated in the absence of the test compound.

In other embodiments, a *ptc* therapeutic of the present invention is one which disrupts the association of *patched* with *smoothed*.

Agonist and antagonists of neuroprotection can be distinguished, and the efficacy of the compound can be assessed, by subsequent testing with neuronal cells.

In an illustrative embodiment, the polypeptide utilized as a *hedgehog* receptor can be generated from the *patched* protein. Accordingly, an exemplary screening assay includes all or a suitable portion of the *patched* protein which can be obtained from, for example, the human *patched* gene (GenBank U43148) or other vertebrate sources (see GenBank Accession numbers U40074 for chicken *patched* and U46155 for mouse *patched*), as well as from *drosophila* (GenBank Accession number M28999) or other invertebrate sources. The *patched* protein can be provided in the screening assay as a whole protein (preferably expressed on the surface of a cell), or alternatively as a fragment of the full length protein which binds to *hedgehog* polypeptides, e.g., as one or both of the substantial extracellular domains (e.g. corresponding to residues Asn120-Ser438 and/or Arg770-Trp1027 of the human *patched* protein). For instance, the *patched* protein can be provided in soluble form, as for example a preparation of one of the extracellular domains, or a preparation of both of the extracellular domains which are covalently connected by an unstructured linker (see, for example, Huston et al. (1988) PNAS 85:4879; and U.S. Patent No. 5,091,513). In other embodiments, the protein can be provided as part of a liposomal preparation or expressed on the surface of a cell. The *patched* protein can be derived from a recombinant gene, e.g., being ectopically expressed in a heterologous cell. For instance, the protein can be expressed on oocytes, mammalian cells (e.g., COS, CHO, 3T3 or the like), or yeast cell by standard recombinant DNA techniques. These recombinant cells can be used for receptor binding, signal transduction or gene expression assays. Marigo et al. (1996) *Development* 122:1225-1233 illustrates a binding assay of human *hedgehog* to chick *patched* protein ectopically expressed in *Xenopus laevis* oocytes. The assay system of Marigo et al. can be adapted to the present drug screening assays. As illustrated in that reference, *Shh* binds to the *patched* protein in a selective, saturable, dose-dependent manner, thus demonstrating that *patched* is a receptor for *Shh*.



Complex formation between the *hedgehog* polypeptide and a *hedgehog* receptor may be detected by a variety of techniques. For instance, modulation of the formation of complexes can be quantitated using, for example, detectably labelled proteins such as radiolabelled, fluorescently labelled, or enzymatically labelled *hedgehog* polypeptides, by immunoassay, or by chromatographic detection.

Typically, for cell-free assays, it will be desirable to immobilize either the *hedgehog* receptor or the *hedgehog* polypeptide to facilitate separation of receptor/*hedgehog* complexes from uncomplexed forms of one of the proteins, as well as to accommodate automation of the assay. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/receptor (GST/receptor) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the *hedgehog* polypeptide, e.g. an  $^{35}\text{S}$ -labeled *hedgehog* polypeptide, and the test compound and incubated under conditions conducive to complex formation, e.g. at physiological conditions for salt and pH, though slightly more stringent conditions may be desired. Following incubation, the beads are washed to remove any unbound *hedgehog* polypeptide, and the matrix bead-bound radiolabel determined directly (e.g. beads placed in scintillant), or in the supernatant after the receptor/*hedgehog* complexes are dissociated. Alternatively, the complexes can be dissociated from the bead, separated by SDS-PAGE gel, and the level of *hedgehog* polypeptide found in the bead fraction quantitated from the gel using standard electrophoretic techniques.

Other techniques for immobilizing proteins on matrices are also available for use in the subject assay. For instance, soluble portions of the *hedgehog* receptor protein can be immobilized utilizing conjugation of biotin and streptavidin. For instance, biotinylated receptor molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with the *hedgehog* receptor but which do not interfere with *hedgehog* binding can be derivatized to the wells of the plate, and the receptor trapped in the wells by antibody conjugation. As above, preparations of a *hedgehog* polypeptide and a test compound are incubated in the receptor-presenting wells of the plate, and the amount of receptor/*hedgehog* complex trapped in the well can be quantitated. Exemplary methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the *hedgehog* polypeptide, or which are reactive with the receptor protein and compete for binding with the *hedgehog* polypeptide; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the *hedgehog* polypeptide. In the instance of

the latter, the enzyme can be chemically conjugated or provided as a fusion protein with the *hedgehog* polypeptide. To illustrate, the *hedgehog* polypeptide can be chemically cross-linked or genetically fused with alkaline phosphatase, and the amount of *hedgehog* polypeptide trapped in the complex can be assessed with a chromogenic substrate of the enzyme, e.g. paranitrophenylphosphate. Likewise, a fusion protein comprising the *hedgehog* polypeptide and glutathione-S-transferase can be provided, and complex formation quantitated by detecting the GST activity using 1-chloro-2,4-dinitrobenzene (Habig et al (1974) *J Biol Chem* 249:7130).

For processes which rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein, such as the anti-*hedgehog* antibodies described herein, can be used. Alternatively, the protein to be detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the *hedgehog* polypeptide or *hedgehog* receptor sequence, a second polypeptide for which antibodies are readily available (e.g. from commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful epitope tags include myc-epitopes (e.g., see Ellison et al. (1991) *J Biol Chem* 266:21150-21157) which includes a 10-residue sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharmacia, NJ).

Where the desired portion of the *hedgehog* receptor (or other *hedgehog* binding molecule) cannot be provided in soluble form, liposomal vesicles can be used to provide manipulatable and isolatable sources of the receptor. For example, both authentic and recombinant forms of the *patched* protein can be reconstituted in artificial lipid vesicles (e.g. phosphatidylcholine liposomes) or in cell membrane-derived vesicles (see, for example, Bear et al. (1992) *Cell* 68:809-818; Newton et al. (1983) *Biochemistry* 22:6110-6117; and Reber et al. (1987) *J Biol Chem* 262:11369-11374).

In addition to cell-free assays, such as described above, the readily available source of *hedgehog* polypeptides provided by the art also facilitates the generation of cell-based assays for identifying small molecule agonists of the neuroprotective activity of wild-type *hedgehog* polypeptides. Analogous to the cell-based assays described above for screening combinatorial libraries, neuronal cells which are sensitive to *hedgehog*-dependent protection, such as dopaminergic and GABAergic neurons, can be contacted with a *hedgehog* polypeptide and a test agent of interest, with the assay scoring for anything from simple binding to the cell to trophic responses by the target cell in the presence and absence of the test agent. As with the cell-free assays, agents which produce a statistically significant change in *hedgehog* activities (either inhibition or potentiation) can be identified.

In other emdodiments, the cell-based assay scores for agents which disrupt association of patched and *smoothened* proteins, e.g., in the cell surface membrane or liposomal preparation.

5 In addition to characterizing cells that naturally express the *patched* protein, cells which have been genetically engineered to ectopically express *patched* can be utilized for drug screening assays. As an example, cells which either express low levels or lack expression of the *patched* protein, e.g. *Xenopus laevis* oocytes, COS cells or yeast cells, can be genetically modified using standard techniques to ectopically express the *patched* protein. (see Marigo et al., *supra*).

10 The resulting recombinant cells, e.g., which express a functional *patched* receptor, can be utilized in receptor binding assays to identify agonist or anatagonsts of *hedgehog* binding. Binding assays can be performed using whole cells. Furthermore, the recombinant cells of the present invention can be engineered to include other heterolgous genes encoding proteins involved in *hedgehog*-dependent siganl pathways. For example, the gene products of one or  
15 more of *smoothened*, *costal-2* and/or *fused* can be co-expressed with *patched* in the reagent cell, with assays being sensitive to the functional reconstituion of the *hedgehog* signal transduction cascade.

Alternatively, liposomal preparations using reconstituted *patched* protein can be utilized. *Patched* protein purified from detergent extracts from both authentic and  
20 recombinant origins can be reconstituted in in artificial lipid vesicles (e.g. phosphatidylcholine liposomes) or in cell membrane-derived vesicles (see, for example, Bear et al. (1992) *Cell* 68:809-818; Newton et al. (1983) *Biochemistry* 22:6110-6117; and Reber et al. (1987) *J Biol Chem* 262:11369-11374). The lamellar structure and size of the resulting liposomes can be characterized using electron microscopy. External orientation of the  
25 *patched* protein in the reconstituted membranes can be demonstrated, for example, by immunoelectron microscopy. The *hedgehog* polypeptide binding activity of liposomes containing *patched* and liposomes without the protein in the presence of candidate agents can be compared in order to identify potential modulators of the *hedgehog-patched* interaction.

The *hedgehog* polypeptide used in these cell-based assays can be provided as a  
30 purified source (natural or recombinant in origin), or in the form of cells/tissue which express the protein and which are co-cultured with the target cells. As in the cell-free assays, where simple binding (rather than induction) is the *hedgehog* activity scored for in the assay, the protein can be labelled by any of the above-mentioned techniques, e.g., fluorescently, enzymatically or radioactively, or detected by immunoassay.

35 In addition to binding studies, functional assays can be used to identified modulators, i.e., agonists of *hedgehog* or *patched* activities. By detecting changes in intracellular signals,

such as alterations in second messengers or gene expression in *patched*-expressing cells contacted with a test agent, candidate antagonists to *patched* signaling can be identified (e.g., having a *hedgehog*-like activity).

5 A number of gene products have been implicated in *patched*-mediated signal transduction, including *patched*, the transcription factor *cubitus interruptus* (*ci*), the serine/threonine kinase *fused* (*fu*) and the gene products of *costal-2*, *smoothened* and *suppressor of fused*.

10 The interaction of a *hedgehog* polypeptide with *patched* sets in motion a cascade involving the activation and inhibition of downstream effectors, the ultimate consequence of which is, in some instances, a detectable change in the transcription or translation of a gene. Potential transcriptional targets of *patched* signaling are the *patched* gene itself (Hidalgo and Ingham, 1990 *Development* 110, 291-301; Marigo et al., 1996 ) and the vertebrate homologs of the drosophila cubitus interruptus gene, the *GLI* genes (Hui et al. (1994) *Dev Biol* 162:402-413). *Patched* gene expression has been shown to be induced in cells of the limb bud and the  
15 neural plate that are responsive to *Shh*. (Marigo et al. (1996) *PNAS*, in press; Marigo et al. (1996) *Development* 122:1225-1233). The *GLI* genes encode putative transcription factors having zinc finger DNA binding domains (Orenic et al. (1990) *Genes & Dev* 4:1053-1067; Kinzler et al. (1990) *Mol Cell Biol* 10:634-642). Transcription of the *GLI* gene has been reported to be upregulated in response to *hedgehog* in limb buds, while transcription of the  
20 *GLI3* gene is downregulated in response to *hedgehog* induction (Marigo et al. (1996) *Development* 122:1225-1233). By selecting transcriptional regulatory sequences from such target genes, e.g. from *patched* or *GLI* genes, that are responsible for the up- or down regulation of these genes in response to *patched* signalling, and operatively linking such promoters to a reporter gene, one can derive a transcription based assay which is sensitive to  
25 the ability of a specific test compound to modify *patched* signalling pathways. Expression of the reporter gene, thus, provides a valuable screening tool for the development of compounds that act as antagonists of *ptc*, e.g., which may be useful as neuroprotective agents.

Reporter gene based assays of this invention measure the end stage of the above described cascade of events, e.g., transcriptional modulation. Accordingly, in practicing one  
30 embodiment of the assay, a reporter gene construct is inserted into the reagent cell in order to generate a detection signal dependent on *ptc* signaling. To identify potential regulatory elements responsive to *ptc* signaling present in the transcriptional regulatory sequence of a target gene, nested deletions of genomic clones of the target gene can be constructed using standard techniques. See, for example, Current Protocols in Molecular Biology, Ausubel,  
35 F.M. et al. (eds.) Greene Publishing Associates, (1989); U.S. Patent 5,266,488; Sato et al. (1995) *J Biol Chem* 270:10314-10322; and Kube et al. (1995) *Cytokine* 7:1-7. A nested set of DNA fragments from the gene's 5'-flanking region are placed upstream of a reporter gene,

such as the luciferase gene, and assayed for their ability to direct reporter gene expression in *patched* expressing cells. Host cells transiently transfected with reporter gene constructs can be scored for the induction of expression of the reporter gene in the presence and absence of *hedgehog* to determine regulatory sequences which are responsive to *patched*-dependent signalling.

5 In practicing one embodiment of the assay, a reporter gene construct is inserted into the reagent cell in order to generate a detection signal dependent on second messengers generated by induction with *hedgehog* polypeptide. Typically, the reporter gene construct will include a reporter gene in operative linkage with one or more transcriptional regulatory elements responsive to the *hedgehog* activity, with the level of expression of the reporter gene providing the *hedgehog*-dependent detection signal. The amount of transcription from the reporter gene may be measured using any method known to those of skill in the art to be suitable. For example, mRNA expression from the reporter gene may be detected using RNAse protection or RNA-based PCR, or the protein product of the reporter gene may be identified by a characteristic stain or an intrinsic activity. The amount of expression from the reporter gene is then compared to the amount of expression in either the same cell in the absence of the test compound (or *hedgehog*) or it may be compared with the amount of transcription in a substantially identical cell that lacks the target receptor protein. Any statistically or otherwise significant difference in the amount of transcription indicates that the test compound has in some manner altered the signal transduction of the *patched* protein, e.g., the test compound is a potential *ptc* therapeutic.

As described in further detail below, in preferred embodiments the gene product of the reporter is detected by an intrinsic activity associated with that product. For instance, the reporter gene may encode a gene product that, by enzymatic activity, gives rise to a detection signal based on color, fluorescence, or luminescence. In other preferred embodiments, the reporter or marker gene provides a selective growth advantage, e.g., the reporter gene may enhance cell viability, relieve a cell nutritional requirement, and/or provide resistance to a drug.

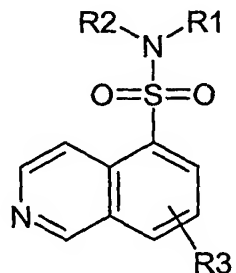
Preferred reporter genes are those that are readily detectable. The reporter gene may also be included in the construct in the form of a fusion gene with a gene that includes desired transcriptional regulatory sequences or exhibits other desirable properties. Examples of reporter genes include, but are not limited to CAT (chloramphenicol acetyl transferase) (Alton and Vapnek (1979), Nature 282: 864-869) luciferase, and other enzyme detection systems, such as beta-galactosidase; firefly luciferase (deWet et al. (1987), Mol. Cell. Biol. 7:725-737); bacterial luciferase (Engebrecht and Silverman (1984), PNAS 1: 4154-4158; Baldwin et al. (1984), Biochemistry 23: 3663-3667); alkaline phosphatase (Toh et al. (1989)

Eur. J. Biochem. 182: 231-238, Hall et al. (1983) J. Mol. Appl. Gen. 2: 101), human placental secreted alkaline phosphatase (Cullen and Malim (1992) Methods in Enzymol. 216:362-368).

Transcriptional control elements which may be included in a reporter gene construct include, but are not limited to, promoters, enhancers, and repressor and activator binding sites. Suitable transcriptional regulatory elements may be derived from the transcriptional regulatory regions of genes whose expression is induced after modulation of a *patched* signal transduction pathway. The characteristics of preferred genes from which the transcriptional control elements are derived include, but are not limited to, low or undetectable expression in quiescent cells, rapid induction at the transcriptional level within minutes of extracellular simulation, induction that is transient and independent of new protein synthesis, subsequent shut-off of transcription requires new protein synthesis, and mRNAs transcribed from these genes have a short half-life. It is not necessary for all of these properties to be present.

In yet other embodiments, second messenger generation can be measured directly in the detection step, such as mobilization of intracellular calcium, phospholipid metabolism or adenylate cyclase activity are quantitated, for instance, the products of phospholipid hydrolysis IP<sub>3</sub>, DAG or cAMP could be measured. For example, recent studies have implicated protein kinase A (PKA) as a possible component of *hedgehog/patched* signaling (Hammerschmidt et al. (1996) *Genes & Dev* 10:647). High PKA activity has been shown to antagonize *hedgehog* signaling in these systems. Conversely, inhibitors of PKA will mimic and/or potentiate the action of *hedgehog*. Although it is unclear whether PKA acts directly downstream or in parallel with *hedgehog* signaling, it is possible that *hedgehog* signalling occurs via inhibition of PKA activity. Thus, detection of PKA activity provides a potential readout for the instant assays.

In a preferred embodiment, the *ptc* therapeutic is a PKA inhibitor. A variety of PKA inhibitors are known in the art, including both peptidyl and organic compounds. For instance, the *ptc* therapeutic can be a 5-isoquinolinesulfonamide, such as represented in the general formula:



wherein,

R<sub>1</sub> and R<sub>2</sub> each can independently represent hydrogen, and as valence and stability permit a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an

ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido,  $-(CH_2)_m-R_8$ ,  $-(CH_2)_m-OH$ ,  $-(CH_2)_m-O$ -lower alkyl,  $-(CH_2)_m-O$ -lower alkenyl,  $-(CH_2)_n-O-(CH_2)_m-R_8$ ,  $-(CH_2)_m-SH$ ,  $-(CH_2)_m-S$ -lower alkyl,  $-(CH_2)_m-S$ -lower alkenyl,  $-(CH_2)_n-S-(CH_2)_m-R_8$ , or

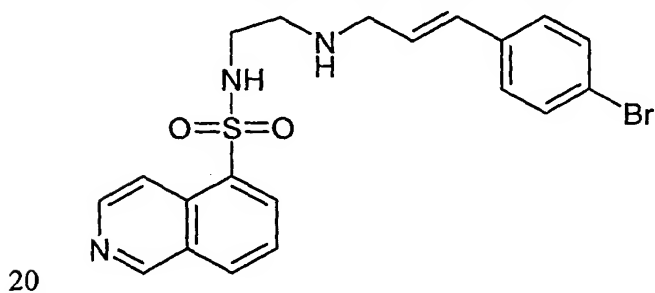
$R_1$  and  $R_2$  taken together with N form a heterocycle (substituted or unsubstituted);

$R_3$  is absent or represents one or more substitutions to the isoquinoline ring such as a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido,  $-(CH_2)_m-R_8$ ,  $-(CH_2)_m-OH$ ,  $-(CH_2)_m-O$ -lower alkyl,  $-(CH_2)_m-O$ -lower alkenyl,  $-(CH_2)_n-O-(CH_2)_m-R_8$ ,  $-(CH_2)_m-SH$ ,  $-(CH_2)_m-S$ -lower alkyl,  $-(CH_2)_m-S$ -lower alkenyl,  $-(CH_2)_n-S-(CH_2)_m-R_8$ ;

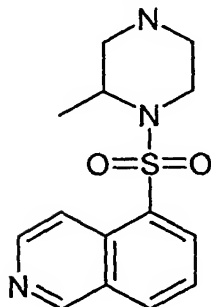
$R_8$  represents a substituted or unsubstituted aryl, aralkyl, cycloalkyl, cycloalkenyl, or heterocycle; and

n and m are independently for each occurrence zero or an integer in the range of 1 to 6.

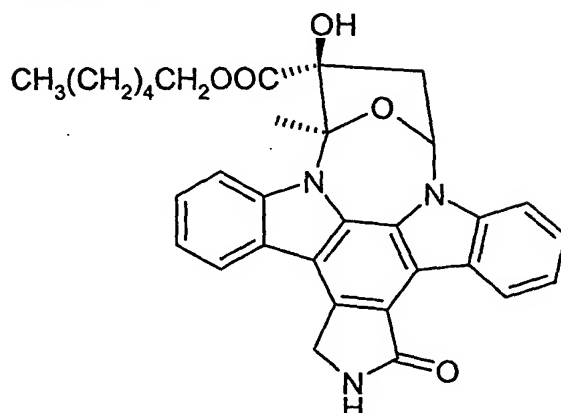
In a preferred embodiment, the PKA inhibitor is N-[2-((p-bromocinnamyl)amino)ethyl]-5-isoquinolinesulfonamide (H-89; Calbiochem Cat. No. 371963), e.g., having the formula:



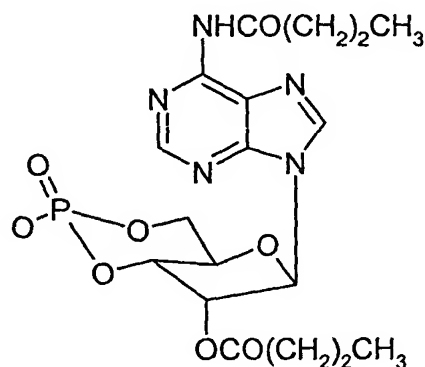
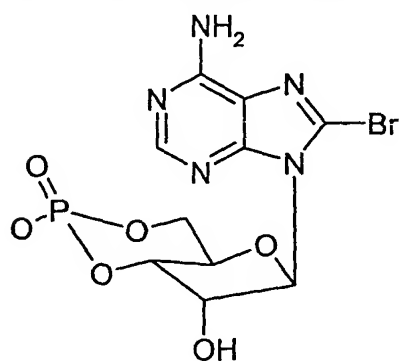
In another embodiment, the PKA inhibitor is 1-(5-isoquinolinesulfonyl)-2-methylpiperazine (H-7; Calbiochem Cat. No. 371955), e.g., having the formula:



In still other embodiments, the PKA inhibitor is KT5720 (Calbiochem Cat. No. 420315), having the structure



A variety of nucleoside analogs are also useful as PKA inhibitors. For example, the subject method can be carried out cyclic AMP analogs which inhibit the kinase activity of PKA, as for example, 8-bromo-cAMP or dibutyryl-cAMP



Exemplary peptidyl inhibitors of PKA activity include the PKA Heat Stable Inhibitor (isoform  $\alpha$ ; see, for example, Calbiochem Cat. No. 539488, and Wen et al. (1995) *J Biol Chem* 270:2041).

Certain *hedgehog* receptors may stimulate the activity of phospholipases. Inositol lipids can be extracted and analyzed using standard lipid extraction techniques. Water soluble derivatives of all three inositol lipids (IP<sub>1</sub>, IP<sub>2</sub>, IP<sub>3</sub>) can also be quantitated using radiolabelling techniques or HPLC.

The mobilization of intracellular calcium or the influx of calcium from outside the cell may be a response to *hedgehog* stimulation or lack thereof. Calcium flux in the reagent cell can be measured using standard techniques. The choice of the appropriate calcium indicator, fluorescent, bioluminescent, metallochromic, or Ca<sup>++</sup>-sensitive microelectrodes depends on the cell type and the magnitude and time constant of the event under study (Borle (1990) *Environ Health Perspect* 84:45-56). As an exemplary method of Ca<sup>++</sup> detection,



cells could be loaded with the  $\text{Ca}^{++}$  sensitive fluorescent dye fura-2 or indo-1, using standard methods, and any change in  $\text{Ca}^{++}$  measured using a fluorometer.

In certain embodiments of the assay, it may be desirable to screen for changes in cellular phosphorylation. As an example, the drosophila gene *fused* (*fu*) which encodes a serine/threonine kinase has been identified as a potential downstream target in *hedgehog* signaling. (Preat et al., 1990 *Nature* 347, 87-89; Therond et al. 1993, *Mech. Dev.* 44. 65-80). The ability of compounds to modulate serine/threonine kinase activation could be screened using colony immunoblotting (Lyons and Nelson (1984) *Proc. Natl. Acad. Sci. USA* 81:7426-7430) using antibodies against phosphorylated serine or threonine residues. Reagents for performing such assays are commercially available, for example, phosphoserine and phosphothreonine specific antibodies which measure increases in phosphorylation of those residues can be purchased from commercial sources.

In yet another embodiment, the *ptc* therapeutic is an antisense molecule which inhibits expression of a protein involved in a *patched*-mediated signal transduction pathway. To illustrate, by inhibiting the expression of a protein involved in *patched* signals, such as *fused*, *costal-2*, *smoothed* and/or *Gli* genes, or *patched* itself, the ability of the patched signal pathway(s) to alter the ability of, e.g., a dopaminergic or GABAergic cell to maintain its differentiated state can be altered, e.g., potentiated or repressed.

As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide probes or their derivatives which specifically hybridize (e.g. bind) under cellular conditions with cellular mRNA and/or genomic DNA encoding a *hedgehog* polypeptide, *patched*, or a protein involved in *patched*-mediated signal transduction. The hybridization should inhibit expression of that protein, e.g. by inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the target cellular mRNA. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a target gene. Such oligonucleotide probes are preferably modified oligonucleotide which are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, and is therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate

analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) *Biotechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668.

5        Several considerations should be taken into account when constructing antisense oligonucleotides for the use in the methods of the invention: (1) oligos should have a GC content of 50% or more; (2) avoid sequences with stretches of 3 or more G's; and (3) oligonucleotides should not be longer than 25-26 mers. When testing an antisense oligonucleotide, a mismatched control can be constructed. The controls can be generated by  
10 reversing the sequence order of the corresponding antisense oligonucleotide in order to conserve the same ratio of bases.

In an illustrative embodiment, the *ptc* therapeutic can be an antisense construct for inhibiting the expression of *patched*, e.g., to mimic the inhibition of *patched* by *hedgehog*. Exemplary antisense constructs include:

15    5'-GTCCTGGCGCCGCCGCCGCGTCGCC  
     5'-TTCCGATGACCGGCCTTTCGCGGTGA  
     5'-GTGCACGGAAAGGTGCAGGCCACACT

#### VI. Exemplary pharmaceutical preparations of *hedgehog* and *ptc* therapeutics

20        The source of the *hedgehog* and *ptc* therapeutics to be formulated will depend on the particular form of the agent. Small organic molecules and peptidyl fragments can be chemically synthesized and provided in a pure form suitable for pharmaceutical/cosmetic usage. Products of natural extracts can be purified according to techniques known in the art. For example, the Cox et al. U.S. Patent 5,286,654 describes a method for purifying naturally  
25 occurring forms of a secreted protein and can be adapted for purification of *hedgehog* polypeptides. Recombinant sources of *hedgehog* polypeptides are also available. For example, the gene encoding *hedgehog* polypeptides, are known, *inter alia*, from PCT publications WO 95/18856 and WO 96/17924.

Those of skill in treating neural tissues can determine the effective amount of an  
30 *hedgehog* or *ptc* therapeutic to be formulated in a pharmaceutical or cosmetic preparation.

The *hedgehog* or *ptc* therapeutic formulations used in the method of the invention are most preferably applied in the form of appropriate compositions. As appropriate compositions there may be cited all compositions usually employed for systemically or locally (such as intrathecal) administering drugs. The pharmaceutically acceptable carrier should be  
35 substantially inert, so as not to act with the active component. Suitable inert carriers include

water, alcohol polyethylene glycol, mineral oil or petroleum gel, propylene glycol and the like.

To prepare the pharmaceutical compositions of this invention, an effective amount of the particular *hedgehog* or *ptc* therapeutic as the active ingredient is combined in intimate admixture with a pharmaceutically acceptable carrier, which carrier may take a wide variety of forms depending on the form of preparation desired for administration. These pharmaceutical compositions are desirable in unitary dosage form suitable, particularly, for administration orally, rectally, percutaneously, or by parenteral injection. For example, in preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed such as, for example, water, glycols, oils, alcohols and the like in the case of oral liquid preparations such as suspensions, syrups, elixirs and solutions; or solid carriers such as starches, sugars, kaolin, lubricants, binders, disintegrating agents and the like in the case of powders, pills, capsules, and tablets. Because of their ease in administration, tablets and capsules represents the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. For parenteral compositions, the carrier will usually comprise sterile water, at least in large part, though other ingredients, for example, to aid solubility, may be included. Injectable solutions, for example, may be prepared in which the carrier comprises saline solution, glucose solution or a mixture of saline and glucose solution. Injectable suspensions may also be prepared in which case appropriate liquid carriers, suspending agents and the like may be employed. Also included are solid form preparations which are intended to be converted, shortly before use, to liquid form preparations. In the compositions suitable for percutaneous administration, the carrier optionally comprises a penetration enhancing agent and/or a suitable wetting agent, optionally combined with suitable additives of any nature in minor proportions, which additives do not introduce a significant deleterious effect on the skin.

It is especially advantageous to formulate the subject compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used in the specification and claims herein refers to physically discrete units suitable as unitary dosages, each unit containing a predetermined quantity of active ingredient calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. Examples of such dosage unit forms are tablets (including scored or coated tablets), capsules, pills, powders packets, wafers, injectable solutions or suspensions, teaspoonfuls, tablespoonfuls and the like, and segregated multiples thereof.

The pharmaceutical preparations of the present invention can be used, as stated above, for the many applications which can be considered cosmetic uses. Cosmetic compositions known in the art, preferably hypoallergic and pH controlled are especially preferred, and include toilet waters, packs, lotions, skin milks or milky lotions. The preparations contain,

besides the *hedgehog* or *ptc* therapeutic, components usually employed in such preparations. Examples of such components are oils, fats, waxes, surfactants, humectants, thickening agents, antioxidants, viscosity stabilizers, chelating agents, buffers, preservatives, perfumes, dyestuffs, lower alkanols, and the like. If desired, further ingredients may be incorporated in the compositions, e.g. antiinflammatory agents, antibacterials, antifungals, disinfectants, vitamins, sunscreens, antibiotics, or other anti-acne agents.

Examples of oils comprise fats and oils such as olive oil and hydrogenated oils; waxes such as beeswax and lanolin; hydrocarbons such as liquid paraffin, ceresin, and squalane; fatty acids such as stearic acid and oleic acid; alcohols such as cetyl alcohol, stearyl alcohol, lanolin alcohol, and hexadecanol; and esters such as isopropyl myristate, isopropyl palmitate and butyl stearate. As examples of surfactants there may be cited anionic surfactants such as sodium stearate, sodium cetylsulfate, polyoxyethylene laurylether phosphate, sodium N-acyl glutamate; cationic surfactants such as stearyldimethylbenzylammonium chloride and stearyltrimethylammonium chloride; ampholytic surfactants such as alkylaminoethylglycine hydrochloride solutions and lecithin; and nonionic surfactants such as glycerin monostearate, sorbitan monostearate, sucrose fatty acid esters, propylene glycol monostearate, polyoxyethylene oleylether, polyethylene glycol monostearate, polyoxyethylene sorbitan monopalmitate, polyoxyethylene coconut fatty acid monoethanolamide, polyoxypropylene glycol (e.g. the materials sold under the trademark "Pluronic"), polyoxyethylene castor oil, and polyoxyethylene lanolin. Examples of humectants include glycerin, 1,3-butylene glycol, and propylene glycol; examples of lower alcohols include ethanol and isopropanol; examples of thickening agents include xanthan gum, hydroxypropyl cellulose, hydroxypropyl methyl cellulose, polyethylene glycol and sodium carboxymethyl cellulose; examples of antioxidants comprise butylated hydroxytoluene, butylated hydroxyanisole, propyl gallate, citric acid and ethoxyquin; examples of chelating agents include disodium edetate and ethanehydroxy diphosphate; examples of buffers comprise citric acid, sodium citrate, boric acid, borax, and disodium hydrogen phosphate; and examples of preservatives are methyl parahydroxybenzoate, ethyl parahydroxybenzoate, dehydroacetic acid, salicylic acid and benzoic acid.

For preparing ointments, creams, toilet waters, skin milks, and the like, typically from 0.01 to 10% in particular from 0.1 to 5% and more in particular from 0.2 to 2.5% of the active ingredient, e.g., of the *hedgehog* or *ptc* therapeutic, will be incorporated in the compositions. In ointments or creams, the carrier for example consists of 1 to 20%, in particular 5 to 15% of a humectant, 0.1 to 10% in particular from 0.5 to 5% of a thickener and water; or said carrier may consist of 70 to 99%, in particular 20 to 95% of a surfactant, and 0 to 20%, in particular 2.5 to 15% of a fat; or 80 to 99.9% in particular 90 to 99% of a thickener; or 5 to 15% of a surfactant, 2-15% of a humectant, 0 to 80% of an oil, very small ( < 2%) amounts of

preservative, coloring agent and/or perfume, and water. In a toilet water, the carrier for example consists of 2 to 10% of a lower alcohol, 0.1 to 10% or in particular 0.5 to 1% of a surfactant, 1 to 20%, in particular 3 to 7% of a humectant, 0 to 5% of a buffer, water and small amounts ( < 2%) of preservative, dyestuff and/or perfume. In a skin milk, the carrier typically consists of 10-50% of oil, 1 to 10% of surfactant, 50-80% of water and 0 to 3% of preservative and/or perfume. In the aforementioned preparations, all % symbols refer to weight by weight percentage.

Particular compositions for use in the method of the present invention are those wherein the *hedgehog* or *ptc* therapeutic is formulated in liposome-containing compositions. Liposomes are artificial vesicles formed by amphiphatic molecules such as polar lipids, for example, phosphatidyl cholines, ethanolamines and serines, sphingomyelins, cardiolipins, plasmalogens, phosphatidic acids and cerebiosides. Liposomes are formed when suitable amphiphatic molecules are allowed to swell in water or aqueous solutions to form liquid crystals usually of multilayer structure comprised of many bilayers separated from each other by aqueous material (also referred to as coarse liposomes). Another type of liposome known to be consisting of a single bilayer encapsulating aqueous material is referred to as a unilamellar vesicle. If water-soluble materials are included in the aqueous phase during the swelling of the lipids they become entrapped in the aqueous layer between the lipid bilayers.

Water-soluble active ingredients such as, for example, various salt forms of a *hedgehog* polypeptide, are encapsulated in the aqueous spaces between the molecular layers. The lipid soluble active ingredient of *hedgehog* or *ptc* therapeutic, such as an organic mimetic, is predominantly incorporated into the lipid layers, although polar head groups may protude from the layer into the aqueous space. The encapsulation of these compounds can be achieved by a number of methods. The method most commonly used involves casting a thin film of phospholipid onto the walls of a flask by evaporation from an organic solvent. When this film is dispersed in a suitable aqueous medium, multilamellar liposomes are formed. Upon suitable sonication, the coarse liposomes form smaller similarly closed vesicles.

Water-soluble active ingredients are usually incorporated by dispersing the cast film with an aqueous solution of the compound. The unencapsulated compound is then removed by centrifugation, chromatography, dialysis or other art-known suitable procedures. The lipid-soluble active ingredient is usually incorporated by dissolving it in the organic solvent with the phospholipid prior to casting the film. If the solubility of the material in the lipid phase is not exceeded or the amount present is not in excess of that which can be bound to the lipid, liposomes prepared by the above method usually contain most of the material bound in the lipid bilayers; separation of the liposomes from unencapsulated material is not required.

A particularly convenient method for preparing liposome formulated forms of *hedgehog* and *ptc* therapeutics is the method described in EP-A-253,619, incorporated herein

by reference. In this method, single bilayered liposomes containing encapsulated active ingredients are prepared by dissolving the lipid component in an organic medium, injecting the organic solution of the lipid component under pressure into an aqueous component while simultaneously mixing the organic and aqueous components with a high speed homogenizer or mixing means, whereupon the liposomes are formed spontaneously.

The single bilayered liposomes containing the encapsulated *hedgehog* or *ptc* therapeutic can be employed directly or they can be employed in a suitable pharmaceutically acceptable carrier for localized administration. The viscosity of the liposomes can be increased by the addition of one or more suitable thickening agents such as, for example xanthan gum, hydroxypropyl cellulose, hydroxypropyl methylcellulose and mixtures thereof. The aqueous component may consist of water alone or it may contain electrolytes, buffered systems and other ingredients, such as, for example, preservatives. Suitable electrolytes which can be employed include metal salts such as alkali metal and alkaline earth metal salts. The preferred metal salts are calcium chloride, sodium chloride and potassium chloride. The concentration of the electrolyte may vary from zero to 260 mM, preferably from 5 mM to 160 mM. The aqueous component is placed in a suitable vessel which can be adapted to effect homogenization by effecting great turbulence during the injection of the organic component. Homogenization of the two components can be accomplished within the vessel, or, alternatively, the aqueous and organic components may be injected separately into a mixing means which is located outside the vessel. In the latter case, the liposomes are formed in the mixing means and then transferred to another vessel for collection purpose.

The organic component consists of a suitable non-toxic, pharmaceutically acceptable solvent such as, for example ethanol, glycerol, propylene glycol and polyethylene glycol, and a suitable phospholipid which is soluble in the solvent. Suitable phospholipids which can be employed include lecithin, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, phosphatidylinositol, lysophosphatidylcholine and phosphatidyl glycerol, for example. Other lipophilic additives may be employed in order to selectively modify the characteristics of the liposomes. Examples of such other additives include stearylamine, phosphatidic acid, tocopherol, cholesterol and lanolin extracts.

In addition, other ingredients which can prevent oxidation of the phospholipids may be added to the organic component. Examples of such other ingredients include tocopherol, butylated hydroxyanisole, butylated hydroxytoluene, ascorbyl palmitate and ascorbyl oleate. Preservatives such as benzoic acid, methyl paraben and propyl paraben may also be added.

Methods of introduction may also be provided by rechargeable or biodegradable devices. Various slow release polymeric devices have been developed and tested *in vivo* in recent years for the controlled delivery of drugs, including proteinacious biopharmaceuticals. A variety of biocompatible polymers (including hydrogels), including both biodegradable and

non-degradable polymers, can be used to form an implant for the sustained release of an *hh* at a particular target site. Such embodiments of the present invention can be used for the delivery of an exogenously purified *hedgehog* polypeptide, which has been incorporated in the polymeric device, or for the delivery of *hedgehog* produced by a cell encapsulated in the polymeric device.

An essential feature of certain embodiments of the implant can be the linear release of the therapeutic, which can be achieved through the manipulation of the polymer composition and form. By choice of monomer composition or polymerization technique, the amount of water, porosity and consequent permeability characteristics can be controlled. The selection of the shape, size, polymer, and method for implantation can be determined on an individual basis according to the disorder to be treated and the individual patient response. The generation of such implants is generally known in the art. See, for example, *Concise Encyclopedia of Medical & Dental Materials*, ed. by David Williams (MIT Press: Cambridge, MA, 1990); and the Sabel et al. U.S. Patent No. 4,883,666.

In another embodiment of an implant, a source of cells producing the therapeutic, e.g., secreting a soluble form of a *hedgehog* polypeptide, is encapsulated in implantable hollow fibers or the like. Such fibers can be pre-spun and subsequently loaded with the cell source (Aebischer et al. U.S. Patent No. 4,892,538; Aebischer et al. U.S. Patent No. 5,106,627; Hoffman et al. (1990) *Expt. Neurobiol.* 110:39-44; Jaeger et al. (1990) *Prog. Brain Res.* 82:41-46; and Aebischer et al. (1991) *J. Biomech. Eng.* 113:178-183), or can be co-extruded with a polymer which acts to form a polymeric coat about the cells (Lim U.S. Patent No. 4,391,909; Sefton U.S. Patent No. 4,353,888; Sugamori et al. (1989) *Trans. Am. Artif. Intern. Organs* 35:791-799; Sefton et al. (1987) *Biotechnol. Bioeng.* 29:1135-1143; and Aebischer et al. (1991) *Biomaterials* 12:50-55).

25

### *Exemplification*

The invention now being generally described, it will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention.

30

**Example I:** *Hedgehog* polypeptides promote survival of specific CNS neuron populations and protect these cells from toxic insult *in vitro*.

In *Drosophila*, the *hedgehog* gene was first discovered for the role it plays in early embryo patterning (Nusslein-Volhard and Wieschaus, 1980). Further study showed tht the product of this gene is secreted, and as an intercellular signaling protein, plays a critical role

35

in body segmentation and patterning of imaginal disc derivatives such as eyes and wings (Lee et al., 1992; Mohler and Vanie, 1992; Tabata et al., 1992). There re, at present, three mammalian homologues of *Drosophila hedgehog*, and Indian *hedgehog* (Fietz et al., 1994). During the course of vertebrate development, these secreted peptide molecules are involved  
5 in axial patterning, and consequently regulate the phenotypic specification of precursor cells into functional differentiated cells.

The embryonic expression pattern of Shh has been shown to be closely linked to the development and differentiation of the entire ventral neuraxis (Marti et al., 1995). Using naive neural tube explants derived from the appropriate levels of the rostrocaudal axis, it has  
10 been demonstrated that the induction of spinal motor neurons (Roelink et al., 1994; Tanabe et al., 1995), midbrain dopaminergic neurons (Hynes et al., 1995; Wang et al., 1995), and basal forebrain cholinergic neurons (Ericson et al., 1995) are dependent upon exposure to Shh. This molecule appears to be crucial for such patterning and phenotype specification in vivo since mouse embryos deficient in the expression of functional Shh gene product manifest a  
15 lack of normal ventral patterning in the central nervous system as well as gross atrophy of the entire cranium (Chiang et al., 1996).

In this study we have explored the issue of whether Shh may have activities at stages in neural development later than those previously studied. Namely, wew have asked whether Shh is trophic for particular neural populations, and under toxic conditions, whethre Shh is  
20 neuroprotective. Using cultures derived from the embryonic day 14-16 (E14-16) rat, we find that Shh is trophic for midbrain, striatial, and spinal neurons. In the first case the factor is trophic for both dopaminergic and GABA-immunoreactive (GABA-ir) neurons. From the striatum, the surviving neurons are exclusively GABA-ir, while in the spinal cultures Shh promotes survival of a heterogeneous population of putative interneurons. Shh does not  
25 suport survival of any peripheral nervous system neurons tested. Finally, we show that Shh protects cultures of midbrain dopaminergic neurons from the toxic effects of MPP+, a specific neurotoxin that induces Parkinsonism *in vivo*. Together, these observations indicate a novel role for Shh in nervous system development and its potential role as a therapeutic.

## 30 Materials and Methods

### *Whole-mount in situ hybridization*

Whole-mount in situ hybridization on bisected E14.5 Sprague-Dawley rat embryos was performed with digoxigenin-labeled (Boehringer-Mannheim) mouse RNA probes as previously described (Wilkinson, 1992). Bound probe was detected with alkaline  
35 phosphatase-conjugated anti-digoxigenin Fab fragments (BoehringerMannheim). The 0.7 kb *Shh* probes were transcribed using T3 (antisense) or T7 (sense) RNA polymerase from *Hind*



*III* (antisense) or *Bam HI* (sense) linearized templates as described by Echelard, et al. (1993). The 0.9 kb *Ptc* probes were transcribed using T3 (antisense) or T7 (sense) RNA polymerase from *Bam HI* (antisense) or *Hind III* (sense) linearized templates as described by Goodrich, et al. (1996).

## 5 *Shh protein and anti-Shh antibody*

Rat sonic *hedgehog* amino terminal signaling domain (amino acids 2-198) Porter et al., 1995) was cloned into a baculovirus expression vector (Invitrogen; San Diego, CA) (virus encoding Shh insert was a gift of Dr. Henk Roelink, University of Washington, Seattle, WA). High Five™ insect cells (Invitrogen) were infected with the baculovirus per manufacturer's instructions. The culture supernatant was batch adsorbed to heparin agarose type I (Sigma; St. Louis, MO) and Shh eluted with PBS containing a total of 0.75 M NaCl and 0.1- mM -mercaptoethanol. Shh concentration was determined by the method of Ericson, et al. (1996). E. coli-derived Shh was obtained as previously described (Wang et al., 1996) and purified as described above. All samples were sterile filtered and aliquots frozen in liquid nitrogen.

Anti-Shh polyclonal antibody was a gift from Dr. Andy McMahon (Harvard University). Preparation of this reagent, directed against the amino peptide of Shh, is described by Bumcrot et al. (1995). Anti-Shh monoclonal antibody (511) was a gift of Dr. Thomas Jessell (Columbia University), and preparation of this reagent is described by Ericson et al. (1996).

## *Dissociation and culture of neural tissue*

E14.5 rat ventral mesencephalon was dissected as described by Shimoda, et al. (Shimoda et al., 1992). Striatal cultures were established from E15-16 embryos from the regions identified by Altman and Bayer (1995) as the striatum and pallidum. Spinal cultures utilized the ventral one-third of the E15-16 spinal cord (Camu and Henderson, 1992). Tissues were dissociated for approximately 40 minutes in 0.10-0.25% trypsin-EDTA (Gibco/BRL; Gaithersburg, MD), and the digestion stopped using an equal volume of Ca++/Mg++-free Hanks' buffered saline (Gibco/BRL) containing 3.5 mg/ml soybean trypsin inhibitor (Sigma) and 0.04% DNase (Grade II, Boehringer Mannheim; Indianapolis, IN). Cells were then plated at  $2 \times 10^5$  -  $3 \times 10^5$  cells/well in the medium of Kriegstein, et al. (1995) (a modified N2 medium) in 34-well tissue culture plates (Falcon) coated with poly-L-lysine or poly-L-ornithine (Sigma) after 2 wash in the same medium. Note that this procedure results in cultures in which the cells have never been exposed to serum and stands in contrast to cultures in which serum has been used to neutralize dissociation proteases, and/or to initially "prime" the cells prior to serum withdrawal. The following peptide growth factors were added as indicated in the results: basic fibroblast growth factor (FGFb), transforming growth factor 1 (TGF 1), TGF 2, glia derived neurotrophic factor (GDNF), and brain derived neurotrophic factor (BDNF) (all from PeproTech; Rocky Hill, NJ; additional lots of BDNF and GDNF were purchased from Promega; Madison WI). Anti-TGF antibodies were

purchased from R & D Systems. Antibody was added at the time of Shh addition to the cultures. Cultures were maintained for up to 3 weeks and the medium changed every 4 days.

#### *Immunocytochemistry and cell scoring*

For all cell staining, cultures were fixed with 5% paraformaldehyde in PBS (plus  
5 0.1% glutaraldehyde if staining for GABA), and blocked using 3% goat serum, (Sigma),  
0.1% Triton X-100, in PBS. Antibody incubations were performed in the blocking solutions.  
Antibodies used in this study were anti-tubulin III (Sigma), anti-tyrosine hydroxylase (TH)  
(Boehringer-Mannheim), anti-GABA (Sigma), and anti-glial fibrillary acidic protein (GFAP)  
(Sigma). Primary antibodies were detected using horseradish peroxidase-, alkaline  
10 phosphatase-, or fluochrome-conjugated secondary antibodies (Vector; Burlingame, CA).  
Peroxidase-linked secondaries were visualized using a NI/DAB kit (Zymed; South San  
Francisco, CA) and phosphatase-linked secondaries using Vector Blue™ (Vector).

Cell counting was performed using an Olympus inverted microscope at a total  
magnification of 300X. Data presented are representative, and have been confirmed by  
15 repeating the cultures at least 4-10 independent times for each neural population discussed.  
Cell numbers are reported as cells/field (the average of 30-40 fields from a total of 5  
wells/condition; 4-10 independent experiments were assessed for each culture condition  
examined). Consistency of counting was verified by at least 3 observers. Errors are reported  
as standard error of the mean (s.e.m.), and significance calculated by student's t-test.

#### 20 *Measurement of dopamine transport*

To detect the presence of the dopamine transporter (Cerruti et al., 1993; Ciliax et al.,  
1995) cultures were incubated with a mixture consisting of:  $5 \times 10^{-8}$ M  $^3$ H-dopamine  
(Amersham; Arlington Heights, IL; 48 Ci/mmol), 100  $\mu$ M ascorbic acid (Sigma), 1  $\mu$ M  
fluoxetine (Eli Lilly; Indianapolis, IN), 1  $\mu$ M desmethylinipramine (Sigma), and 10  $\mu$ M  
25 pargyline (Sigma) in DME-F12. Nonspecific labeling was measured by the addition of  $5 \times$   
 $10^{-5}$ M unlabeled dopamine. Cells were incubated for 30 minutes at 37 °C, rinsed three times  
with PBS and processed for either scintillation counting or autoradiography. For scintillation  
counting cells were first lysed with 150  $\mu$ l of 0.1% SDS and then added to 500  $\mu$ l of  
Microscint 20 (Packard; Meriden, CT) and counted in a Packard Instrument Topcount  
30 scintillation machine. For autoradiography, sister plates were coated with NTB-2  
autoradiographic emulsion (Kodak; Rochester, NY) that had been diluted 1:3 with 10%  
glycerol. The plates were then air dried, exposed for 1-2 weeks, and developed.

#### *Quantitative-competitive polymerase chain reaction (QC-PCR)*

RNA was isolated from cells and tissue using Trizol (Gibco/BRL) as prescribed by  
35 the manufacturer. Genomic DNA was removed from the RNA by incubation with 0.5 units  
of Dnase (Gibco/BRL, Cat # 28068-015) at room temperature for 25 minutes. The solution

was heated to 75 C for 20 minutes to inactivate the DNase. Reverse transcription was carried out using random hexamer and MuLV reverse transcriptase (Gibco/BRL) as suggested by the manufacturer. All the quantitative RT-PCR internal controls, or mimics, were synthetic single stranded DNA oligonucleotides corresponding to the target sequence with an internal deletion from the central region (Oligos, Etc.; Wilsonville, OR). For actin, target = 280 bp, mimic = 230 bp; for *ptc*, target = 354 bp, mimic = 200 bp. PCR was performed using the Clontech PCR kit. For actin: annealing temperature 64 C, oligos GGCTCCGGTATGTGC, GGGGTACTTCAGGGT. For *ptc*: annealing temperature 72 C, oligos CATTGGCAGGAGGAGTTGATTGTGG, AGCACCTTTTGAGTGGAGTTTGGGG. In each QC-PCR reaction, four reactions were set up with equal amounts of sample cDNA in each tube and 5-fold serial dilution of mimic. Also, for each sample an aliquot of cDNA was saved and amplified along with quantitative PCR as control for contamination. PCR reactions were carried out in an MJ Research PTC-200 thermal cycler and the following cycling profile used: 95 C for 45 seconds, 64 or 72 C for 35 seconds, 82 C for 30 seconds; for 40 cycles. The reaction mixtures were then fractionated by agarose electrophoresis, negative films obtained, and the films digitally scanned and quantified by area integration according to established procedures (Wang et al., 1995, and references therein). The quantity of target molecules was normalized to the competing mimic and expressed as a function of cDNA synthesized and used in each reaction.

#### 20 *N-methyl-4-phenylpyrrolidinium (MPP+) administration*

Culture and MPP+ treatment of dopaminergic neurons were performed as previously described (Hyman et al., 1994; Kriegstein et al., 1995). MPP+ (Aldrich; St. Louis, MO) was added at day 3 of culture to a final concentration of 3  $\mu$ M for 58 hours. Cultures were then washed extensively to remove MPP+, cultured for an additional 34-48 hours to allow clearance of dying TH+ neurons, and then processed for immunocytochemistry.

## Results

### *Shh and Ptc Continue to be Expressed in the Rat CNS After the Major Period of Dorsoventral Patterning*

Previous studies have shown that *shh* is expressed in the vertebrate embryo in the period during which dorsoventral patterning manifests (approximately E9-10 in the rat). Within the central nervous system, *shh* expression persists beyond this period and can be detected at a very high level in the E14-16 rat embryo. For example, in situ hybridization studies of the E14.5 embryo (Fig. 1A and E) reveal that *shh* is expressed in ventral regions of the spinal cord, hindbrain, midbrain, and diencephalon. Lower levels of expression are observed in the ventral striatum and septum, while no expression is observed in the cortex

within the limits of detection of this method. Interestingly, a “streak” of *shh* expression (Fig. 1A, arrow) is observed to bisect the diencephalon into rostral and caudal halves. This is likely to be the zona limitans intrathalamica that separates prosomeres 2 and 3, and has been previously observed in the studies of *shh* expression in the developing chick embryo (Marti, et al., 1995).

Recent biochemical evidence supports the view that the *ptc* gene product can act as a high affinity Shh receptor (Marigo et al., 1996a; Stone et al., 1996). *Ptc* shows a complementary pattern of expression (Fig. 1C and E), and is observed primarily lateral and dorsal to the sites of *shh* expression. The complementarity of expression is most dramatic in the diencephalon where *ptc* mRNA is absent from the zona limitans, but is expressed at a very high level on either side of this structure. Of further interest is the observation that rostral of the zonal limitans, *ptc* expression no longer seems as restricted to regions immediately dorsal of *shh* expression. Again, within the detection limits of this technique, *ptc* is not expressed in the cortex. Thus in regions where *shh* is expressed, adjacent tissue appears capable of responding to the gene product as evidenced by expression of the putative receptor.

#### *Shh Promotes Dopaminergic Neuron Survival*

In the developing midbrain (E9), Shh was first characterized for its ability to induce the production of dopaminergic neurons. Thus the trophic potential of Shh was tested on this neuronal population at a stage when these neurons have already been induced. Using cultures derived from the E14.5 mesencephalon it was found that Shh increases the survival of TH+ neurons in a dose dependent manner (Fig. 2A). These cells exhibited a neuronal morphology (Fig. 2B), and greater than 95% of the TH+ cells were also positive for the neuron-specific marker, tubulin III (Banerjee et al., 1990); GFAP staining revealed no glial cells (data not shown). Differences in TH+ neuron survival between control and Shh treated wells could be observed as early as 5 days. Note that under these stringently serum-free conditions (i.e. at no time were the cells exposed to serum), baseline levels of survival are even lower than those conventionally reported for cultures that have been maintained in low serum or that have been briefly serum “primed”. By 3 weeks in culture less than 6% of the total TH+ cells plated were present in the control condition, whereas 35-30% survive at 60 ng/ml of Shh (from 5 to 24 days,  $p < .001$  at 35 and 60 ng/ml).

All catecholaminergic neurons express TH, but the presence of a specific high affinity DA uptake system is indicative of midbrain dopaminergic neurons (Di Porzio et al., 1980; Denis-Donini et al., 1984; Cerruti et al., 1993; Ciliax et al., 1995). As further evidence that the cells supported by Shh are *bone fide* dopaminergic neurons, specific, high affinity dopamine (DA) uptake was also demonstrated (Figure 3). Midbrain cultures treated with Shh transported and retained  $^3\text{H}$ -DA with a dose response profile paralleling that of survival

curves (Fig. 3A) ( $p < 0.005$  at 25 and 50 ng/ml). Emulsion autoradiography also demonstrated that the cells taking up  $^3\text{H}$ -DA were neuronal in morphology (Fig. 3B). In addition, immunohistochemistry for dopamine itself demonstrated high cellular content (data not shown).

5        The observed effect of Shh on increased TH+ neuron number is unlikely to be due to differentiation of latent progenitor cells since previous studies demonstrated that the ability of Shh to induce dopaminergic neurons in explanted tissue is lost at later stages of development (Hynes et al., 1995; Wang et al., 1995). Furthermore, the effects are unlikely to be due to a mitogenic response of committed neuroblasts since pulsing the cultures with 5-bromp-2'-  
10    deoxyuridine (BrdU) at 1, 2, or 4 days *in vitro* revealed very low mitotic activity in the presence or absence of Shh (data not shown). Thus in addition to inducing dopaminergic neurons in the naive mesencephalon, Shh is a trophic factor for these neurons.

*Specificity of Shh Action on Midbrain Neurons: Regulated expression of Ptc*

Expression of *ptc* has previously been shown to be regulated by Shh (Goodrich et al.,  
15    1996; Marigo et al., 1996b), and to date, Shh is the only factor known to transcriptionally upregulate *ptc* expression. Therefore, the expression of *ptc* by mesencephalic explants would reinforce the view that these cells are capable of responding to Shh, and upregulation of *ptc* mRNA in response to Shh would strongly indicate the specificity of such a response. Therefore, quantitative competitive PCR (QC-PCR) was used to measure the level of *ptc*  
20    expression.

*Ptc* mRNA levels were measured at 0, 3, 5, and 7 days of culture by the method described by Wang, et al. (1995). For each culture condition at each timepoint, 5 separate cDNA samples were co-amplified with a different known amount of mimic substrate (DNA that can be amplified by the same primers but yielding a product of molecular weight lower  
25    than that being sought in the sample). Thus for each condition and timepoint, a gel like that shown in Fig. 4A was generated (upper bands correspond to amplified *ptc* transcripts; lower bands correspond to amplified mimic). Using a scanning densitometer to quantify the observed bands, a graph was produced for each sample (Fig. 4B corresponds to Fig. 4A). When the density of the target band and the mimic band are equal, the concentration of the  
30    unknown target can be taken to be equal to the known concentration of mimic. Based on a linear curve fit, the concentration of mimic at the point at which the density of the mimic and the target substrate are equal ( $\text{Log } D_s/D_m = 0$ ) was taken to be the concentration of the substrate in the sample; this value was then normalized to the total amount of cDNA added to the reaction. These values are plotted in Fig. 4C; correlation coefficients ( $r^2$ ) of the curve fits  
35    always exceeded 0.95, and thus the margin of error for the values presented is less than 5%. This experiment was performed two independent times with independent cultures and the results were nearly identical.

As shown in Fig. 4C, significant *ptc* expression was observed in the E14.5 ventral mesencephalon (time 0). After two days of culture, higher levels of *ptc* expression were observed than at the time of dissection; in control cultures this might reflect the loss of *ptc* non-expressing cell types since a constant amount of RNA was analyzed. There was no  
 5 difference in *ptc* expression between control cultures and those treated with either 5 or 25 ng/ml of Shh at this time. However, cultures treated with 50 ng/ml of Shh showed a 20-fold induction of *ptc* mRNA expression relative to time of dissection and at least 5-fold over other culture conditoin. By 5 days of culture, *ptc* message levels had declined significantly in comparison to the 3 day level of expression but high levels of expression were still observed  
 10 in 50 ng/ml Shh. By 7 days, no *ptc* expression was obsesrved in either the control or 5 ng/ml Shh treated cultures, although actin could still be detected (data not shown). It is important to note that in the 25 and 50 ng/ml Shh-treated cultures *ptc* expression matched or exceeded the time zero expression of *ptc* in the mesencephalon despite the overall decrease in cell number. These results indicate that: A) *ptc* is expressed in the E14.5 ventral mesencephalon  
 15 (suggesting that the cells in this region are capable of responding to Shh), b) Shh is necessary for the maintenance of *ptc* gene expression, and c) that the expression of *ptc* shows a Shh dose dependence that parallels the neurotrophic activity described above.

#### *Specificity of Shh Action on Midbrain Neurons: Immunoneutralization*

As further evidence that the trophic activity of Shh preparation used for these studies,  
 20 purified from a baculovirus expression system, was due to Shh and not to a contaminating factor, antibody neutralization experiments were performed. As shown in Fig. 4D, a saturating dose of Shh (50 ng/ml) promotes midbrain neuron survival ( $p < .001$ ) while the same dose of Shh in the presence of a 5-fold molar excess of activity-neutralizgin, anti-Shh, monoclonal antibody (5E1; Ericson, et al. (1996)) inhibits this trophic response ( $p < .001$ ). In  
 25 earlier studies (data not shown), an affinity purified, polyclonal, anti-Shh antibody dramatically reduced the activity of Shh in the dopaminergic neuron survival assay ( $p < .005$ ), whereas purified rabbit IgG antibody from preimmune sera had no significant effect. Anti-TGF antibodies used at a 3-fold molar excess to Shh did not inhibit the trophic activity, while they did inhibit the previously reported (Krieglestein et al., 1995) trophic effects of  
 30 exogenously applied TGF s (data not shown). Addition of -galactosidase, expressed and purified in a manner identical to Shh, failed to show any trophic effect (data not shown), and thus renders unlikely the possibility that an undefined baculovirus protein iss responsible for the observed trophic effects. Finally, Shh purified from an *E. coli* expression system (Wang et al., 1995) also had trophic activity for Th+ cells, while -galactosidase purified identically  
 35 to Shh from the *E. coli* expression system gave no such activity even at concentrations as high as 20  $\mu$ g/ml (data not shown).

#### *Shh supports the Survival of other Midbrain Neurons*

Since the original observations concerning the role of Shh in midbrain development were concerned with induction of dopaminergic neurons (Hynes et al., 1995; Want et al., 1995), the current study initially focused on possible trophic effects on these neurons. Interestingly, the cultures in which the above described trophic effects were observed, also demonstrated that the trophic effect of Shh extended to non-dopaminergic neurons (i.e. TH neurons). Within the dopaminergic nucleus of the midbrain, the substantia nigra, GABA is also a major neurotransmitter (Masuko et al., 1992). Staining for GABA in these cultures (Fig. 5) showed that GABA+ cells are supported by the presence of Shh with a dose response profile comparable to TH+ cells. Furthermore, GABA cells outnumbered TH+ cells by a ratio of approximately 3.1. The two cell types together account for approximately 95% of the total neurons as gauged by staining for tubulin III (data not shown), and thus it is clear that the trophic effect of Shh on midbrain neurons extends to multiple neuron subtypes (for TH,  $p < 0.001$  at 35 and 60 ng/ml; for GABA,  $p < .001$  at 35 and 60 ng/ml).

#### *Shh Effects on Striatal Neurons*

Since Shh is strongly expressed in the ventral and lateral forebrain (Echelard et al., 1993; Ericson et al., 1995), and that the Shh knockout mouse exhibits striatal defects (Chiang et al., 1996), Shh neurotrophic activity was examined in striatum-derived cultures as well. As assessed after 4 days *in vitro* (Fig. 6), Shh is a potent trophic factor for neurons cultured from the E15-16 striatum, and shows a dose response comparable to that of the midbrain. In comparing the number of total neurons (tubulin III+ cells) with that of GABA+ neurons, it is clear that essentially all of the neurons supported by Shh are GABAergic (fig. 6) (tubulin III,  $p < 0.001$  at 25 and 50 ng/ml; GABA,  $p < .001$  at 25 and 50 ng/ml). That this effect is strictly trophic was confirmed by the observation that BrdU labeling indices over the course of the culture period were low and did not vary with dose (data not shown). Closer inspection reveals that the intensity of GABA staining is variable, and it is thus possible that various subtypes of GABA+ interneurons (reviewed by Kawaguchi et al., 1995) are all supported by Shh.

#### *Shh Effects on Spinal Neurons*

As a further examination of the postinductive effectiveness of Shh on ventral neural tube derivatives, cultures of the E14-15 ventral neural tube were cultured with varying amounts of Shh. Again, with a dose response identical to that observed in the mesencephalic and striatal cultures, Shh promotes the survival of tubulin III+ neurons as scored after 4 days *in vitro* (Fig. 6A). A majority, but not all of these cells also stain for GABA, and a smaller subset stain for a nuclear marker of spinal interneurons, Lim-1/2 (Tsuchida et al., 1994) (Fig 6A-C) (tubulin III,  $p < 0.001$  at 25 and 50 ng/ml; Lim-1/2,  $p < .001$  at 5, 10, 25 and 50 ng/ml; GABA,  $p .001$  at 25 and 50 ng/ml). It is important to note that while there is overlap between the GABA+ and Lim-1/2+ populations, the latter is not merely a subset of the former since

there are Lim-1/2+ cells that do not stain for GABA. Interestingly, immunoreactivity for the low affinity nerve growth factor receptor (Camu and Henderson, 1992), Islet-1 (Ericson et al., 1992), or galectin-1 (Hynes et al., 1990), all markers of rat motoneurons, was not detectable in these cultures, and thus it appears that Shh is not trophic for spinal motoneurons.

#### 5 *Shh Protects Th+ Cells Against MPP+ Toxicity*

The toxin, 5-phenyl-1,2,3,6-tetrahydropterine (MPTP), and its active metabolite, MPP+, are selectively toxic to mesencephalic dopaminergic neurons (Kopin and Markey, 1988; Forno et al., 1993). Since other agents that promote survival of TH+ cells also protect against chemical toxicity of MPP+ (Hyman et al., 1991; Kriegstein et al., 1995), we tested the ability of Shh to protect TH+ cells in E14 rat mesencephalon explants from the effects of MPP+. As shown in Figure 8, the presence of Shh in cultures treated for 58 hours with MPP+ significantly increased the numbers of TH+ cells that were observed in culture after removal of the MPP+. MPP+ treatment caused a greater than 90% reduction in the numbers of TH+ cells compared to non-MPP+ treated control cultures, whereas incubation with Shh protected the Th+ cells so that only a 75% reduction of TH+ cells occurred after MPP+ treatment versus controls. Sister cultures tested for 4H-DA transport demonstrated a 8-fold increase in transport in Shh treated cultures versus controls (data not shown).

Shh was significantly more active in protecting TH+ cells from the effects of MPP+ than the other growth factors tested: glia-derived neurotrophic factor (GDNF) (Lin et al., 1993) and brain-derived neurotrophic factor (BDNF) (Hyman et al., 1991) (Shh,  $p < 0.001$  at 60 and 350 ng/ml; BDNF no significance; GDNF,  $p < .05$ ). In the serum free conditions used in these experiments, none of the other growth factors tested showed as significant a level of TH+ cell protection from MPP+ toxicity as Shh, even when tested at levels previously shown to be optimal for neuroprotection (Fig. 8).

25

## **Discussion**

### *Shh is Neurotrophic for a Variety of Ventral Neurons*

The hypothesis that Shh may play roles in the nervous system in addition to its initial function in neural tube ventralization was first suggested by the observation that Shh expression in ventral neural tissue along the entire neuraxis continues well past the period during which phenotypic specification has occurred (Echelard et al., 1993). Moreover, preliminary evidence generated in our laboratory indicates the presence of significant levels of *Shh* mRNA in specific regions of the adult human-CNS (e.g. spinal cord and substantia nigra, P. Jin, unpublished observations). We report here the first evidence that Shh can indeed exert effects independent of its induction and patterning activity.

35



Unlike its role at earlier stages of neural development, this novel neurotrophic activity acts on postmitotic neurons rather than on dividing progenitor cells. While the general trophic effect is apparent in a number of CNS regions (Fig. 2 and 6-7), there are both differences and similarities in the effects observed among the regions examined. Given the fact that Shh is necessary for the induction of both spinal motor neurons and midbrain dopaminergic neurons, one might predict that Shh would be subsequently trophic for the cells. Strikingly, Shh is a very potent trophic factor for the midbrain dopaminergic neurons (Fig. 2), but in the cultures of ventral spinal neurons, no such effect on motor neurons was observed. Thus there is no direct correlation between the neuron phenotypes induced by Shh, and those supported by Shh in a trophic manner. Interestingly, a common feature among the three CNS regions examined was the trophic effect for GABAergic neurons (Fig. 6-7). While it is not obvious whether these specific GABA<sup>+</sup> populations are directly or indirectly induced by Shh during early development (cf. Pfaff et al., 1996), it is plausible that the trophic actions on these neurons are direct.

It is important to note that the neurotrophic effects reported herein are not lacking in specificity. For example, neurons of the peripheral nervous system show no survival in response to Shh administration, and preliminary studies of cultures derived from E15-16 dorsal CNS regions (e.g. neocortex and dorsal spinal cord) show high baseline levels of neuron survival with no significant response to exogenous Shh application (J.A.O. and N.K.M., unpublished observation). Thus there appears to be a general restriction of the trophic effects of Shh to regions of the CNS specified by Shh, but the actual targets of trophic activity need not encompass the phenotypes whose induction is Shh-dependent. Nevertheless, the fact that Shh also protects neurons from toxic insult (Fig. 8), suggests previously unforeseen therapeutic roles for Shh as well.

#### *Possible Mechanisms of Shh Action*

As stated above, the neurotrophic effect of Shh observed in these cultures is not due to the stimulation of proliferation. One could argue, however, that the observed effects are indirect. In one scenario, Shh may act on a non-neuronal cell that in turn responds by secreting a neurotrophic factor. We observed no sign of astrocytes in any of our neural cultures, either by morphology or by staining for GFAP. Furthermore, in the purely neuronal cultures established from the midbrain, *ptc* is greatly upregulated in response to Shh, and thus the reported survival effects must be due to a response by neurons (Fig. 4C).

In another scenario, it is possible that Shh acts directly on some or all of the neurons, but the response is to secrete another factor(s) that actually possesses the survival activity. For example, Shh has been shown to induce the expression of TGF family members such as BMP's *in vivo* (Laufer et al., 1994; Levin et al., 1995) and these proteins are trophic for midbrain dopaminergic neurons (Kriegstein et al., 1995). That induced expression of TGF s

is the trophic mechanism seems unlikely since exogenous TGF s show only modest trophic activity in our culture system, and the presence of neutralizing, anti-pan-TGF antibodies failed to inhibit the neurotrophic effects of Shh. Thus, at a minimum, Shh supports the survival of a subset of ventral CNS neurons. The mechanism by which Shh supports neuron survival is yet to be determined. While we favor the hypothesis that these trophic effects are direct, it remains possible that the survival response is due to Shh-induced expression of a secondary trophic factor.

As in the case of many secreted peptide factors, it now appears that Shh has activities that can vary greatly depending on the spatiotemporal context in which the factor is expressed. While it was initially thought that the primary role of Shh in the CNS is in early patterning events that are critical to phenotypic specification, it is now clear that Shh can also contribute to the survival and maturation of these CNS regions. Interestingly, the cell types acted upon in these two distinct roles of Shh do not necessarily overlap. Thus a more thorough understanding of this multifaceted molecule will require a better understanding of its patterns of expression beyond early embryogenesis. Moreover, it will be critical to ascertain the significance of the trophic effects of Shh *in vivo*.

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5    **Example 2: Restoration of function paradigm - establishment of a stable lesion through administration of 6-OHDA with subsequent administration of Shh.**

These experiments analyzed reduction in toxin-induced asymmetry of nigrostriatal system as examined by apomorphine induced rotational behaviors.

10    Briefly, Fisher 344 rats were injected with 6-OHDA into the right medial forebrain bundle. Male rats were anesthetized with 400 mg/kg chloral hydrate injected intraperitoneally and placed in a stereotaxic frame. The skin over the skull was retracted; a burr hole was then placed in the skull over the lesion site and a needle attached to a microliter syringe was lowered into the medial forebrain bundle (4.4 mm posterior to bregma, 1.3 mm lateral, 7.8 mm ventral to the dural surface). 9 ug/4 ul/4 min of 6-hydroxydopamine (6-  
15    OHDA) in ascorbate was then injected. The needle was withdrawn after one additional minute and the surgical wound was closed with skin clips.

All lesioned animals exhibited a stable rotation pattern and turned >300 times contralateral to the lesion after a low dose of apomorphine. Prior to intracranial injections of Shh (N-terminal fragment, unmodified, E. coli recombinant) or vehicle, all rats showed a  
20    slight increase in apomorphine-induced rotations as measured at weekly intervals for the 3 weeks prior to administration of test solution.

In order to achieve a more uniform distribution of Shh, two stereotactically guided injections of 5 ul each were made at distinct sites within the substantia nigra. With the incisor bar positioned to -2.3 mm, the injection coordinates based on bregma (Paxinos and  
25    Watson, 1986) were as follows: Site 1: AP -5.6 mm, ML -1.87, DV -7.3 mm; site 2: AP -5.6mm, ML -2.5 mm, DV -6.8 mm. Incisions were closed using stainless steel wound clips, and the animals were allowed to recover for 1 week before subsequent behavioral testing.

Figures 9 and 10 illustrate the restorative activity of Shh on apomorphine-induced lesioned rats.

30

**Example 3: Neuroprotective paradigm - simultaneous administration of 6-OHDA and Shh.**

This set of experiments analyzed protection from toxin-induced asymmetry of the nigrostriatal system as examined by amphetamine induced rotational behavior.

Briefly, at day 0, animals were injected with 6-OHDA unilaterally into their medial forebrain bundle at coordinates -2.8 mm from bregma, 2 mm lateral to the midline and 8.6 mm below the skull. Similarly, the animals were injected with Shh (N-terminal fragment, unmodified E. coli recombinant, 10 µg) or vehicle unilaterally into SNc/VTA at coordinates -4.8 mm from bregma, 1.4 mm lateral to the midline, and 8.2 mm below the skull. Coordinates according to the atlas of Paxinos and Watson (1986).

At day 4, the animals were challenged with amphetamines and ipsiversive rotations were measured. Figures 11A and 11B demonstrate the neuroprotective activity of Shh.

#### 10 **Example 4:** Further animal studies of neuroprotective effect of Shh.

As with example 3, this set of experiments analyzed protection from toxin-induced asymmetry of the nigrostriatal system as examined by amphetamine induced rotational behavior.

At Day 0, 6-OHDA was unilaterally injected into the medial forebrain bundle at coordinates -2.8mm from bregma, 2mm lateral to the midline and 8.6mm below the skull. The animals were also injected, into the lateral SNc at coordinates -4.8mm from bregma, 1.4mm lateral to the midline and 8.2mm below the skull, with vehicle ("X-treated"), or with one of two doses of Shh (N-terminal fragment, unmodified E. coli recombinant), 30 µg ("Y-treated") or 10 µg ("Z-treated"). Coordinates according to the atlas of Paxinos and Watson (1986).

At days 4, 7, 14 and 21, the animals were challenged with amphetamines and ipsiversive rotations were measured. The animals were also challenged on day 24 with apomorphine. Figures 14A-E demonstrate the dose-dependent neuroprotective activity of Shh.

#### 25 **Example 5:** Neuroprotective Activity of lipophilic-modified Shh.

Utilizing the protocol of Example 4, animals were treated with either vehicle ("C-treated"), or 76ng ("A-treated") or 760ng ("B-treated") of a myristoylated N-terminal fragment of Shh. At days 4, 7, 14 and 21, the animals were challenged with amphetamines and ipsiversive rotations were measured. The animals were also challenged on day 24 with apomorphine. Figures 15A-H demonstrate the dose-dependent neuroprotective activity of Shh. Figure 16 is a collective graph of the data, specifically the ipsilateral turns over 21 days after 6-OHDA treatment, and indicates that myristoylated Shh protects against 6-OHDA lesions.

**Example 6: Restoration of function paradigm - comparison of myristoylated and unmyristoylated Shh.**

These experiments compared reduction in toxin-induced asymmetry of the nigrostriatal system, as examined by apomorphine and amphetamine induced rotational behaviors, for various forms of *hedgehog* polypeptides, namely lipid-modified and unmodified forms of the proteins. See, e.g., Pepinsky et al. (1998) *JBC* 273:14037 for a discussion of lipid-modified *hedgehog* polypeptides.

Animals were prepared in a similar fashion to the 6-OHDA lesioned rats of Example 2. Briefly, each rat was given a dose of desipramine HCl (25 mg/kg i.p.) and pargyline (50 mg/kg i.p.), and anesthetized with isoflurane in oxygen. After shaving the scalp, the head was fixed in a stereotaxic frame according to the atlas of Paxinos and Watson (1986). A midline longitudinal incision was made, and the skin flap retracted to reveal the surface of the skull. With the aid of an operating microscope, a small burr-hole was drilled overlaying the left medial forebrain bundle (stereotaxic coordinates: AP +5.2 mm from interaural line (or AP -3.8 mm from bregma); L 1.0 mm). The tip of an injection cannula (backfilled with injectate) was lowered to a depth of 8.0 mm below the surface of the brain so that the tip is located in the medial forebrain bundle, and was left in place for 5 min before the injection. 6-Hydroxydopamine hydrobromide (1.5 or 6 µg in 2 µl) was injected over 5 min, with the cannula left in place for a further 5 min. After removal of the cannula the burr-hole was sealed bone wax, and the scalp wound closed with sutures.

*Apomorphine (Contralateral) Circling Tests (Days 14, 22, 30 and 38)*

An 8-channel Rotometry System (Benwick Electronics, Wimblington, U.K.) was used for the circling tests. Apomorphine HCl and amphetamine HCl were dissolved in sterile water for injection. For each test, rats were dosed with apomorphine HCl (0.3 mg/kg i.p.), placed in a swivel-harness in rotometry bowls (diameter 24 cm), and left in the bowls for 45 min. Clockwise and anticlockwise rotations were logged automatically.

*Amphetamine (Ipsilateral) Circling Tests (Days 15, 23, 31 and 39)*

The rats were placed in a rotometry bowl (as above) prior to injection of amphetamine HCl (1 mg/kg i.p.). Immediately after injection, they were placed in the rotometer harness and left in the bowls for 120 min. Clockwise and anticlockwise rotations were logged automatically.

*Microinjection of Shh or Vehicle (Day 21)*



Each rat was anesthetized with halothane (1.3% in oxygen) and, after shaving the scalp, the head was fixed in a stereotaxic frame according to the atlas of Paxinos and Watson (1986). A longitudinal incision was made, offset to the left of the midline, and the skin flap retracted to reveal the surface of the skull. With the aid of an operating microscope, a small burr-hole was drilled overlying the left substantia nigra (stereotaxic coordinates AP -5.6 mm from bregma; L 2.0 mm). The tip of an injection cannula (backfilled with injectate) was lowered to a depth of 7.3 mm below the brain surface so that the tip was located dorsal to the middle of the substantia nigra, and was left in place for 5 min before the injection. The injectate (1  $\mu$ l of solution Gz or Mz) was injected over 5 min, and the cannula left in place for a further 5 min. After removal of the cannula, the burr hole was sealed with bone wax, the scalp wound closed with sutures, and the anesthesia discontinued.

Figures 12 and 13 demonstrate an increased potency, as a restorative agent, of a myristoylated form of Shh (Mz) relative to the unmodified form of the protein (Gz).

**Example 7: Evaluating the Efficacy of Human Sonic *Hedgehog* polypeptide Constructs in a Rat Model of Huntington's Disease**

Injection of malonate, an inhibitor of the mitochondrial enzyme succinate dehydrogenase, into the rat striatum (the rodent equivalent of the primate caudate and putamen) causes degeneration of striatal medium spiny neurons. In humans, degeneration of medium spiny neurons in the caudate and putamen is the primary pathological feature of Huntington's disease. Thus, the malonate-induced striatal lesion in rats can be used as a model to test whether human *hedgehog* polypeptides can prevent the death of the neurons that degenerate in Huntington's disease.

Sprague-Dawley rats are injected with various concentrations of *hedgehog* polypeptide in the striatum using stereotaxic techniques. Stereotaxic injections (2  $\mu$ l) are done under sodium pentobarbital anesthesia (40 mg/kg) and placed at the following coordinates: 0.7 mm anterior to bregma, 2.8 mm lateral to the midline and 5.5 mm ventral to the surface of the skull at bregma. At various times (usually 48 hr) after injection of *hedgehog* polypeptide, rats are anesthetized with isoflurane and given a stereotaxic injection of malonate (2  $\mu$ mol in 2  $\mu$ l) at the same coordinates in the striatum. Four days after malonate injection, rats are sacrificed and their brains removed for histological analysis. Coronal sections are cut through the striatum at a thickness of 25  $\mu$ m and stained for cytochrome oxidase activity to distinguish lesioned from unlesioned tissue. The volume of the lesion in the striatum is measured using image analysis.

The effect of sonic *hedgehog* polypeptide constructs given 48 hours before malonate is shown in Figure 17. Unmodified sonic *hedgehog* polypeptide (Shh), myristoylated Shh,

C1II-Shh and octyl maleimide Shh all reduce lesion volume to a similar extent in this model. However, the hydrophobically modified proteins (myristoylated Shh, C1II-Shh and octyl maleimide Shh) show an increase in potency relative to the unmodified sonic *hedgehog* polypeptide. Figure 18 shows the time course for the effect of pretreatment with myristoylated Shh (0.5  $\mu$ g in 2  $\mu$ l) in the malonate striatal lesion model. A statistically significant reduction in lesion volume is seen when myristoylated Shh is given 2 days before malonate, however myristoylated Shh has a greater effect when given either 3 or 4 days before malonate. There was not a statistically significant reduction in lesion volume when myristoylated Shh was given 1 day, 7 days or immediately (0 days) before malonate.

All of the above-cited references and publications are hereby incorporated by reference.

#### *Equivalents*

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

## SEQUENCE LISTING

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 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1277 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 10 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
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 (B) LOCATION: 1..1275  
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10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1190 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1191

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	275 280 285	
50	GTG TTC GCG CGC CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC	912
	Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly	
	290 295 300	
55	GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA	960
	Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu	
	305 310 315 320	
60	GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC	1008
	Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val	
	325 330 335	
65	AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG	1056
	Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp	
	340 345 350	
70	GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT	1104
	Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala	
	355 360 365	

	CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT	1152	
	Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser		
	370 375 380		
5	CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG	1190	
	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly		
	385 390 395		
10	(2) INFORMATION FOR SEQ ID NO:3:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 1281 base pairs		
	(B) TYPE: nucleic acid		
15	(C) STRANDEDNESS: both		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: cDNA		
20	(ix) FEATURE:		
	(A) NAME/KEY: CDS		
	(B) LOCATION: 1..1233		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:		
	ATG TCT CCC GCC TGG CTC CGG CCC CGA CTG CGG TTC TGT CTG TTC CTG	48	
	Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu		
30	1 5 10 15		
	CTG CTG CTG CTT CTG GTG CCG GCG GCG CGG GGC TGC GGG CCG GGC CGG	96	
	Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg		
	20 25 30		
35	GTG GTG GGC AGC CGC CGG AGG CCG CCT CGC AAG CTC GTG CCT CTT GCC	144	
	Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala		
	35 40 45		
40	TAC AAG CAG TTC AGC CCC AAC GTG CCG GAG AAG ACC CTG GGC GCC AGC	192	
	Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser		
	50 55 60		
	GGG CGC TAC GAA GGC AAG ATC GCG CGC AGC TCT GAG CGC TTC AAA GAG	240	
45	Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu		
	65 70 75 80		
	CTC ACC CCC AAC TAC AAT CCC GAC ATC ATC TTC AAG GAC GAG GAG AAC	288	
	Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn		
50	85 90 95		
	ACG GGT GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGT CTG AAC	336	
	Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn		
	100 105 110		
55	TCA CTG GCC ATC TCT GTC ATG AAC CAG TGG CCT GGT GTG AAA CTG CGG	384	
	Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg		
	115 120 125		
60	GTG ACC GAA GGC CGG GAT GAA GAT GGC CAT CAC TCA GAG GAG TCT TTA	432	

	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	
	130						135					140					
5	CAC	TAT	GAG	GGC	CGC	GCG	GTG	GAT	ATC	ACC	ACC	TCA	GAC	CGT	GAC	CGA	480
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	
	145					150					155					160	
10	AAT	AAG	TAT	GGA	CTG	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	GAC	528
	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	
					165					170					175		
15	TGG	GTG	TAT	TAC	GAG	TCC	AAG	GCC	CAC	GTG	CAT	TGC	TCT	GTC	AAG	TCT	576
	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	His	Val	His	Cys	Ser	Val	Lys	Ser	
				180					185					190			
	GAG	CAT	TCG	GCC	GCT	GCC	AAG	ACA	GGT	GGC	TGC	TTT	CCT	GCC	GGA	GCC	624
	Glu	His	Ser	Ala	Ala	Ala	Lys	Thr	Gly	Gly	Cys	Phe	Pro	Ala	Gly	Ala	
			195					200					205				
20	CAG	GTG	CGC	CTA	GAG	AAC	GGG	GAG	CGT	GTG	GCC	CTG	TCA	GCT	GTA	AAG	672
	Gln	Val	Arg	Leu	Glu	Asn	Gly	Glu	Arg	Val	Ala	Leu	Ser	Ala	Val	Lys	
		210					215					220					
25	CCA	GGA	GAC	CGG	GTG	CTG	GCC	ATG	GGG	GAG	GAT	GGG	ACC	CCC	ACC	TTC	720
	Pro	Gly	Asp	Arg	Val	Leu	Ala	Met	Gly	Glu	Asp	Gly	Thr	Pro	Thr	Phe	
	225					230					235					240	
30	AGT	GAT	GTG	CTT	ATT	TTC	CTG	GAC	CGC	GAG	CCA	AAC	CGG	CTG	AGA	GCT	768
	Ser	Asp	Val	Leu	Ile	Phe	Leu	Asp	Arg	Glu	Pro	Asn	Arg	Leu	Arg	Ala	
				245						250					255		
35	TTC	CAG	GTC	ATC	GAG	ACT	CAG	GAT	CCT	CCG	CGT	CGG	CTG	GCG	CTC	ACG	816
	Phe	Gln	Val	Ile	Glu	Thr	Gln	Asp	Pro	Pro	Arg	Arg	Leu	Ala	Leu	Thr	
				260					265					270			
	CCT	GCC	CAC	CTG	CTC	TTC	ATT	GCG	GAC	AAT	CAT	ACA	GAA	CCA	GCA	GCC	864
	Pro	Ala	His	Leu	Leu	Phe	Ile	Ala	Asp	Asn	His	Thr	Glu	Pro	Ala	Ala	
			275					280					285				
40	CAC	TTC	CGG	GCC	ACA	TTT	GCC	AGC	CAT	GTG	CAA	CCA	GGC	CAA	TAT	GTG	912
	His	Phe	Arg	Ala	Thr	Phe	Ala	Ser	His	Val	Gln	Pro	Gly	Gln	Tyr	Val	
		290					295					300					
45	CTG	GTA	TCA	GGG	GTA	CCA	GGC	CTC	CAG	CCT	GCT	CGG	GTG	GCA	GCT	GTC	960
	Leu	Val	Ser	Gly	Val	Pro	Gly	Leu	Gln	Pro	Ala	Arg	Val	Ala	Ala	Val	
	305					310					315					320	
50	TCC	ACC	CAC	GTG	GCC	CTT	GGG	TCC	TAT	GCT	CCT	CTC	ACA	AGG	CAT	GGG	1008
	Ser	Thr	His	Val	Ala	Leu	Gly	Ser	Tyr	Ala	Pro	Leu	Thr	Arg	His	Gly	
					325					330					335		
55	ACA	CTT	GTG	GTG	GAG	GAT	GTG	GTG	GCC	TCC	TGC	TTT	GCA	GCT	GTG	GCT	1056
	Thr	Leu	Val	Val	Glu	Asp	Val	Val	Ala	Ser	Cys	Phe	Ala	Ala	Val	Ala	
				340					345					350			
	GAC	CAC	CAT	CTG	GCT	CAG	TTG	GCC	TTC	TGG	CCC	CTG	CGA	CTG	TTT	CCC	1104
	Asp	His	His	Leu	Ala	Gln	Leu	Ala	Phe	Trp	Pro	Leu	Arg	Leu	Phe	Pro	
			355					360					365				
60	AGT	TTG	GCA	TGG	GGC	AGC	TGG	ACC	CCA	AGT	GAG	GGT	GTT	CAC	TCC	TAC	1152



	Ser	Leu	Ala	Trp	Gly	Ser	Trp	Thr	Pro	Ser	Glu	Gly	Val	His	Ser	Tyr	
	370						375					380					
5	CCT	CAG	ATG	CTC	TAC	CGC	CTG	GGG	CGT	CTC	TTG	CTA	GAA	GAG	AGC	ACC	1200
	Pro	Gln	Met	Leu	Tyr	Arg	Leu	Gly	Arg	Leu	Leu	Leu	Glu	Glu	Ser	Thr	
	385					390					395				400		
10	TTC	CAT	CCA	CTG	GGC	ATG	TCT	GGG	GCA	GGA	AGC	TGAAGGGACT	CTAACCACTG				1253
	Phe	His	Pro	Leu	Gly	Met	Ser	Gly	Ala	Gly	Ser						
				405					410								
	CCCTCCTGGA	ACTGCTGTGC	GTGGATCC														1281
15	(2) INFORMATION FOR SEQ ID NO:4:																
	(i) SEQUENCE CHARACTERISTICS:																
	(A) LENGTH: 1313 base pairs																
20	(B) TYPE: nucleic acid																
	(C) STRANDEDNESS: both																
	(D) TOPOLOGY: linear																
	(ii) MOLECULE TYPE: cDNA																
25	(ix) FEATURE:																
	(A) NAME/KEY: CDS																
	(B) LOCATION: 1..1314																
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:																
	ATG	CTG	CTG	CTG	CTG	GCC	AGA	TGT	TTT	CTG	GTG	ATC	CTT	GCT	TCC	TCG	48
35	Met	Leu	Leu	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Val	Ile	Leu	Ala	Ser	Ser	
	1				5					10				15			
	CTG	CTG	GTG	TGC	CCC	GGG	CTG	GCC	TGT	GGG	CCC	GGC	AGG	GGG	TTT	GGA	96
	Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	
40				20					25					30			
	AAG	AGG	CGG	CAC	CCC	AAA	AAG	CTG	ACC	CCT	TTA	GCC	TAC	AAG	CAG	TTT	144
	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	
			35				40						45				
45	ATT	CCC	AAC	GTA	GCC	GAG	AAG	ACC	CTA	GGG	GCC	AGC	GGC	AGA	TAT	GAA	192
	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	
		50				55						60					
	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAA	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	240
50	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	
	65				70					75				80			
	TAC	AAC	CCC	GAC	ATC	ATA	TTT	AAG	GAT	GAG	GAA	AAC	ACG	GGA	GCA	GAC	288
55	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	
				85					90					95			
	CGG	CTG	ATG	ACT	CAG	AGG	TGC	AAA	GAC	AAG	TTA	AAT	GCC	TTG	GCC	ATC	336
	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
60				100					105					110			

	TCT GTG ATG AAC CAG TGG CCT GGA GTG AGG CTG CGA GTG ACC GAG GGC	384
	Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	
	115 120 125	
5	TGG GAT GAG GAC GGC CAT CAT TCA GAG GAG TCT CTA CAC TAT GAG GGT	432
	Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly	
	130 135 140	
10	CGA GCA GTG GAC ATC ACC ACG TCC GAC CGG GAC CGC AGC AAG TAC GGC	480
	Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly	
	145 150 155 160	
15	ATG CTG GCT CGC CTG GCT GTG GAA GCA GGT TTC GAC TGG GTC TAC TAT	528
	Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
	165 170 175	
20	GAA TCC AAA GCT CAC ATC CAC TGT TCT GTG AAA GCA GAG AAC TCC GTG	576
	Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val	
	180 185 190	
25	GCG GCC AAA TCC GGC GGC TGT TTC CCG GGA TCC GCC ACC GTG CAC CTG	624
	Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu	
	195 200 205	
30	GAG CAG GGC GGC ACC AAG CTG GTG AAG GAC TTA CGT CCC GGA GAC CGC	672
	Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg	
	210 215 220	
35	GTG CTG GCG GCT GAC GAC CAG GGC CGG CTG CTG TAC AGC GAC TTC CTC	720
	Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu	
	225 230 235 240	
40	ACC TTC CTG GAC CGC GAC GAA GGC GCC AAG AAG GTC TTC TAC GTG ATC	768
	Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile	
	245 250 255	
45	GAG ACG CTG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG	816
	Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu	
	260 265 270	
50	CTC TTC GTG GCG CCG CAC AAC GAC TCG GGG CCC ACG CCC GGG CCA AGC	864
	Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser	
	275 280 285	
55	GCG CTC TTT GCC AGC CGC GTG CGC CCC GGG CAG CGC GTG TAC GTG GTG	912
	Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val	
	290 295 300	
60	GCT GAA CGC GGC GGG GAC CGC CGG CTG CTG CCC GCC GCG GTG CAC AGC	960
	Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser	
	305 310 315 320	
65	GTG ACG CTG CGA GAG GAG GAG GCG GGC GCG TAC GCG CCG CTC ACG GCG	1008
	Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala	
	325 330 335	
70	CAC GGC ACC ATT CTC ATC AAC CGG GTG CTC GCC TCG TGC TAC GCT GTC	1056
	His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val	
	340 345 350	

	ATC GAG GAG CAC AGC TGG GCA CAC CGG GCC TTC GCG CCT TTC CGC CTG	1104
	Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu	
	355 360 365	
5	GCG CAC GCG CTG CTG GCC GCG CTG GCA CCC GCC CGC ACG GAC GGC GGG	1152
	Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly	
	370 375 380	
10	GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC	1200
	Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly	
	385 390 395 400	
15	GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC	1248
	Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His	
	405 410 415	
20	ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG	1296
	Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met	
	420 425 430	
25	GCG GTC AAG TCC AGC TG	1313
	Ala Val Lys Ser Ser	
	435	
	(2) INFORMATION FOR SEQ ID NO:5:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 1256 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: cDNA	
	(ix) FEATURE:	
40	(A) NAME/KEY: CDS	
	(B) LOCATION: 1..1257	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
45	ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC	48
	Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser	
	1 5 10 15	
50	TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA	96
	Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg	
	20 25 30	
55	AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
	35 40 45	
60	CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC	192
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
	50 55 60	
60	AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC	240

	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	Tyr	
	65					70					75					80	
5	AAT	CCC	GAC	ATT	ATC	TTT	AAG	GAT	GAG	GAG	AAC	ACG	GGA	GCG	GAC	AGG	288
	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	Arg	
					85				90						95		
10	CTC	ATG	ACA	CAG	AGA	TGC	AAA	GAC	AAG	CTG	AAC	TCG	CTG	GCC	ATC	TCT	336
	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ser	Leu	Ala	Ile	Ser	
				100				105						110			
15	GTA	ATG	AAC	CAC	TGG	CCA	GGG	GTT	AAG	CTG	CGT	GTG	ACA	GAG	GGC	TGG	384
	Val	Met	Asn	His	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	Trp	
			115				120						125				
	GAT	GAG	GAC	GGT	CAC	CAT	TTT	GAA	GAA	TCA	CTC	CAC	TAC	GAG	GGA	AGA	432
	Asp	Glu	Asp	Gly	His	His	Phe	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	
		130					135					140					
20	GCT	GTT	GAT	ATT	ACC	ACC	TCT	GAC	CGA	GAC	AAG	AGC	AAA	TAC	GGG	ACA	480
	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Lys	Ser	Lys	Tyr	Gly	Thr	
	145					150					155					160	
25	CTG	TCT	CGC	CTA	GCT	GTG	GAG	GCT	GGA	TTT	GAC	TGG	GTC	TAT	TAC	GAG	528
	Leu	Ser	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	
				165					170						175		
30	TCC	AAA	GCC	CAC	ATT	CAT	TGC	TCT	GTC	AAA	GCA	GAA	AAT	TCG	GTT	GCT	576
	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	
				180					185					190			
35	GCG	AAA	TCT	GGG	GGC	TGT	TTC	CCA	GGT	TCG	GCT	CTG	GTC	TCG	CTC	CAG	624
	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Leu	Val	Ser	Leu	Gln	
			195					200					205				
	GAC	GGA	GGA	CAG	AAG	GCC	GTG	AAG	GAC	CTG	AAC	CCC	GGA	GAC	AAG	GTG	672
	Asp	Gly	Gly	Gln	Lys	Ala	Val	Lys	Asp	Leu	Asn	Pro	Gly	Asp	Lys	Val	
		210					215					220					
40	CTG	GCG	GCA	GAC	AGC	GCG	GGA	AAC	CTG	GTG	TTC	AGC	GAC	TTC	ATC	ATG	720
	Leu	Ala	Ala	Asp	Ser	Ala	Gly	Asn	Leu	Val	Phe	Ser	Asp	Phe	Ile	Met	
	225					230					235					240	
45	TTC	ACA	GAC	CGA	GAC	TCC	ACG	ACG	CGA	CGT	GTG	TTT	TAC	GTC	ATA	GAA	768
	Phe	Thr	Asp	Arg	Asp	Ser	Thr	Thr	Arg	Arg	Val	Phe	Tyr	Val	Ile	Glu	
				245						250					255		
50	ACG	CAA	GAA	CCC	GTT	GAA	AAG	ATC	ACC	CTC	ACC	GCC	GCT	CAC	CTC	CTT	816
	Thr	Gln	Glu	Pro	Val	Glu	Lys	Ile	Thr	Leu	Thr	Ala	Ala	His	Leu	Leu	
				260					265					270			
55	TTT	GTC	CTC	GAC	AAC	TCA	ACG	GAA	GAT	CTC	CAC	ACC	ATG	ACC	GCC	GCG	864
	Phe	Val	Leu	Asp	Asn	Ser	Thr	Glu	Asp	Leu	His	Thr	Met	Thr	Ala	Ala	
			275					280					285				
	TAT	GCC	AGC	AGT	GTC	AGA	GCC	GGA	CAA	AAG	GTG	ATG	GTT	GTT	GAT	GAT	912
	Tyr	Ala	Ser	Ser	Val	Arg	Ala	Gly	Gln	Lys	Val	Met	Val	Val	Asp	Asp	
		290					295					300					
60	AGC	GGT	CAG	CTT	AAA	TCT	GTC	ATC	GTG	CAG	CGG	ATA	TAC	ACG	GAG	GAG	960

	Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	
	305 310 315 320	
5	CAG CGG GGC TCG TTC GCA CCA GTG ACT GCA CAT GGG ACC ATT GTG GTC Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	1008
	325 330 335	
10	GAC AGA ATA CTG GCG TCC TGT TAC GCC GTA ATA GAG GAC CAG GGG CTT Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	1056
	340 345 350	
15	GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	1104
	355 360 365	
20	TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	1152
	370 375 380	
25	AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	1200
	385 390 395 400	
30	TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	1248
	405 410 415	
35	TCA AGC TG Ser Ser	1256

(2) INFORMATION FOR SEQ ID NO:6:

35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1425 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
45	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 1..1425	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG	48
	Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
	1 5 10 15	
55	CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG	96
	Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
	20 25 30	
60	AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	

		35				40						45						
5	CCC Pro	AAT Asn	GTG Val	GCC Ala	GAG Glu	AAG Lys	ACC Thr	CTA Leu	GGC Gly	GCC Ala	AGC Ser	GGA Gly	AGG Arg	TAT Tyr	GAA Glu	GGG Gly	192	
		50					55					60						
10	AAG Lys	ATC Ile	TCC Ser	AGA Arg	AAC Asn	TCC Ser	GAG Glu	CGA Arg	TTT Phe	AAG Lys	GAA Glu	CTC Leu	ACC Thr	CCC Pro	AAT Asn	TAC Tyr	240	
		65				70					75					80		
15	AAC Asn	CCC Pro	GAC Asp	ATC Ile	ATA Ile	TTT Phe	AAG Lys	GAT Asp	GAA Glu	GAA Glu	AAC Asn	ACC Thr	GGA Gly	GCG Ala	GAC Asp	AGG Arg	288	
					85					90					95			
20	CTG Leu	ATG Met	ACT Thr	CAG Gln	AGG Arg	TGT Cys	AAG Lys	GAC Asp	AAG Lys	TTG Leu	AAC Asn	GCT Ala	TTG Leu	GCC Ala	ATC Ile	TCG Ser	336	
				100					105					110				
25	GTG Val	ATG Met	AAC Asn	CAG Gln	TGG Trp	CCA Pro	GGA Gly	GTG Val	AAA Lys	CTG Leu	CGG Arg	GTG Val	ACC Thr	GAG Glu	GGC Gly	TGG Trp	384	
			115				120						125					
30	GAC Asp	GAA Glu	GAT Asp	GGC Gly	CAC His	CAC His	TCA Ser	GAG Glu	GAG Glu	TCT Ser	CTG Leu	CAC His	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	432	
		130					135					140						
35	GCA Ala	GTG Val	GAC Asp	ATC Ile	ACC Thr	ACG Thr	TCT Ser	GAC Asp	CGC Arg	GAC Asp	CGC Arg	AGC Ser	AAG Lys	TAC Tyr	GGC Gly	ATG Met	480	
		145				150					155					160		
40	CTG Leu	GCC Ala	CGC Arg	CTG Leu	GCG Ala	GTG Val	GAG Glu	GCC Ala	GGC Gly	TTC Phe	GAC Asp	TGG Trp	GTG Val	TAC Tyr	TAC Tyr	GAG Glu	528	
				165					170						175			
45	TCC Ser	AAG Lys	GCA Ala	CAT His	ATC Ile	CAC His	TGC Cys	TCG Ser	GTG Val	AAA Lys	GCA Ala	GAG Glu	AAC Asn	TCG Ser	GTG Val	GCG Ala	576	
				180					185					190				
50	GCC Ala	AAA Lys	TCG Ser	GGA Gly	GGC Gly	TGC Cys	TTC Phe	CCG Pro	GGC Gly	TCG Ser	GCC Ala	ACG Thr	GTG Val	CAC His	CTG Leu	GAG Glu	624	
			195					200					205					
55	CAG Gln	GGC Gly	GGC Gly	ACC Thr	AAG Lys	CTG Leu	GTG Val	AAG Lys	GAC Asp	CTG Leu	AGC Ser	CCC Pro	GGG Gly	GAC Asp	CGC Arg	GTG Val	672	
		210					215					220						
60	CTG Leu	GCG Ala	GCG Ala	GAC Asp	GAC Asp	CAG Gln	GGC Gly	CGG Arg	CTG Leu	CTC Leu	TAC Tyr	AGC Ser	GAC Asp	TTC Phe	CTC Leu	ACT Thr	720	
		225				230					235					240		
65	TTC Phe	CTG Leu	GAC Asp	CGC Arg	GAC Asp	GAC Asp	GGC Gly	GCC Ala	AAG Lys	AAG Lys	GTC Val	TTC Phe	TAC Tyr	GTG Val	ATC Ile	GAG Glu	768	
				245					250						255			
70	ACG Thr	CGG Arg	GAG Glu	CCG Pro	CGC Arg	GAG Glu	CGC Arg	CTG Leu	CTG Leu	CTC Leu	ACC Thr	GCC Ala	GCG Ala	CAC His	CTG Leu	CTC Leu	816	
				260				265						270				
75	TTT Phe	GTG Val	GCG Ala	CCG Pro	CAC His	AAC Asn	GAC Asp	TCG Ser	GCC Ala	ACC Thr	GGG Gly	GAG Glu	CCC Pro	GAG Glu	GCG Ala	TCC Ser	864	

	275	280	285	
5	TCG GGC TCG GGG CCG CCT TCC GGG GGC GCA CTG GGG CCT CGG GCG CTG Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu 290 295 300			912
10	TTC GCC AGC CGC GTG CGC CCG GGC CAG CGC GTG TAC GTG GTG GCC GAG Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu 305 310 315 320			960
15	CGT GAC GGG GAC CGC CGG CTC CTG CCC GCC GCT GTG CAC AGC GTG ACC Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr 325 330 335			1008
20	CTA AGC GAG GAG GCC GCG GGC GCC TAC GCG CCG CTC ACG GCC CAG GGC Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly 340 345 350			1056
25	ACC ATT CTC ATC AAC CGG GTG CTG GCC TCG TGC TAC GCG GTC ATC GAG Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu 355 360 365			1104
30	GAG CAC AGC TGG GCG CAC CGG GCC TTC GCG CCC TTC CGC CTG GCG CAC Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His 370 375 380			1152
35	GCG CTC CTG GCT GCA CTG GCG CCC GCG CGC ACG GAC CGC GGC GGG GAC Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp 385 390 395 400			1200
40	AGC GGC GGC GGG GAC CGC GGG GGC GGC GGC GGC AGA GTA GCC CTA ACC Ser Gly Gly Gly Asp Arg Gly Gly Gly Gly Gly Arg Val Ala Leu Thr 405 410 415			1248
45	GCT CCA GGT GCT GCC GAC GCT CCG GGT GCG GGG GCC ACC GCG GGC ATC Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile 420 425 430			1296
50	CAC TGG TAC TCG CAG CTG CTC TAC CAA ATA GGC ACC TGG CTC CTG GAC His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp 435 440 445			1344
55	AGC GAG GCC CTG CAC CCG CTG GGC ATG GCG GTC AAG TCC AGC NNN AGC Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser 450 455 460			1392
60	CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala 465 470 475			1425

## (2) INFORMATION FOR SEQ ID NO:7:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1622 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: linear
- 60

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

(A) NAME/KEY: CDS

(B) LOCATION: 51..1283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10

CATCAGCCCA CCAGGAGACC TCGCCCGCCG CTCCCCCGGG CTCCCCGGCC ATG TCT 56  
Met Ser  
1

15

CCC GCC CGG CTC CGG CCC CGA CTG CAC TTC TGC CTG GTC CTG TTG CTG 104  
Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu  
5 10 15

20

CTG CTG GTG GTG CCC GCG GCA TGG GGC TGC GGG CCG GGT CGG GTG GTG 152  
Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val  
20 25 30

25

GGC AGC CGC CGG CGA CCG CCA CGC AAA CTC GTG CCG CTC GCC TAC AAG 200  
Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys  
35 40 45 50

30

CAG TTC AGC CCC AAT GTG CCC GAG AAG ACC CTG GGC GCC AGC GGA CGC 248  
Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg  
55 60 65

35

TAT GAA GGC AAG ATC GCT CGC AGC TCC GAG CGC TTC AAG GAG CTC ACC 296  
Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr  
70 75 80

40

CCC AAT TAC AAT CCA GAC ATC ATC TTC AAG GAC GAG GAG AAC ACA GGC 344  
Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly  
85 90 95

45

GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG 392  
Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu  
100 105 110

50

GCT ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC 440  
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr  
115 120 125 130

GAG GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT 488  
Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr  
135 140 145

55

GAG GGC CGC GCG GTG GAC ATC ACC ACA TCA GAC CGC GAC CGC AAT AAG 536  
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys  
150 155 160

60

TAT GGA CTG CTG GCG CGC TTG GCA GTG GAG GCC GGC TTT GAC TGG GTG 584  
Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val  
165 170 175

TAT TAC GAG TCA AAG GCC CAC GTG CAT TGC TCC GTC AAG TCC GAG CAC 632  
Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His



	180	185	190	
5	TCG GCC GCA GCC AAG ACG GGC GGC TGC TTC CCT GCC GGA GCC CAG GTA Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val 195 200 205 210	680		
10	CGC CTG GAG AGT GGG GCG CGT GTG GCC TTG TCA GCC GTG AGG CCG GGA Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly 215 220 225	728		
15	GAC CGT GTG CTG GCC ATG GGG GAG GAT GGG AGC CCC ACC TTC AGC GAT Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp 230 235 240	776		
20	GTG CTC ATT TTC CTG GAC CGC GAG CCC CAC AGG CTG AGA GCC TTC CAG Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln 245 250 255	824		
25	GTC ATC GAG ACT CAG GAC CCC CCA CGC CGC CTG GCA CTC ACA CCC GCT Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala 260 265 270	872		
30	CAC CTG CTC TTT ACG GCT GAC AAT CAC ACG GAG CCG GCA GCC CGC TTC His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe 275 280 285 290	920		
35	CGG GCC ACA TTT GCC AGC CAC GTG CAG CCT GGC CAG TAC GTG CTG GTG Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val 295 300 305	968		
40	GCT GGG GTG CCA GGC CTG CAG CCT GCC CGC GTG GCA GCT GTC TCT ACA Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr 310 315 320	1016		
45	CAC GTG GCC CTC GGG GCC TAC GCC CCG CTC ACA AAG CAT GGG ACA CTG His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu 325 330 335	1064		
50	GTG GTG GAG GAT GTG GTG GCA TCC TGC TTC GCG GCC GTG GCT GAC CAC Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Val Ala Asp His 340 345 350	1112		
55	CAC CTG GCT CAG TTG GCC TTC TGG CCC CTG AGA CTC TTT CAC AGC TTG His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu 355 360 365 370	1160		
60	GCA TGG GGC AGC TGG ACC CCG GGG GAG GGT GTG CAT TGG TAC CCC CAG Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln 375 380 385	1208		
65	CTG CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser Phe His 390 395 400	1256		
70	CCA CTG GGC ATG TCC GGG GCA GGG AGC TGAAAGGACT CCACCGCTGC Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410	1303		
75	CCTCCTGGAA CTGCTGTACT GGGTCCAGAA GCCTCTCAGC CAGGAGGGAG CTGGCCCTGG	1363		

AAGGGACCTG AGCTGGGGGA CACTGGCTCC TGCCATCTCC TCTGCCATGA AGATACACCA 1423  
 TTGAGACTTG ACTGGGCAAC ACCAGCGTCC CCCACCCGCG TCGTGGTGTA GTCATAGAGC 1483  
 5 TGCAAGCTGA GCTGGCGAGG GGATGGTTGT TGACCCCTCT CTCCTAGAGA CCTTGAGGCT 1543  
 GGCACGGCGA CTCCCAACTC AGCCTGCTCT CACTACGAGT TTTCATACTC TGCCTCCCCC 1603  
 ATTGGGAGGG CCCATTCCC 1622

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 1191 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1191

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG 48  
 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu  
 1 5 10 15  
 35 GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG 96  
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
 20 25 30  
 40 CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT 144  
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
 35 40 45  
 45 GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG 192  
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
 50 55 60  
 50 GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CGG GAC CTC GTG CCC AAC 240  
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn  
 65 70 75 80  
 55 TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC 288  
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp  
 85 90 95  
 60 CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT 336  
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile  
 100 105 110  
 GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC 384  
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
 115 120 125

60

	TGG	GAC	GAG	GAC	GGC	CAC	CAC	GCT	CAG	GAT	TCA	CTC	CAC	TAC	GAA	GGC	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	
		130					135					140					
5	CGT	GCT	TTG	GAC	ATC	ACT	ACG	TCT	GAC	CGC	GAC	CGC	AAC	AAG	TAT	GGG	480
	Arg	Ala	Leu	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	
	145					150					155					160	
10	TTG	CTG	GCG	CGC	CTC	GCA	GTG	GAA	GCC	GGC	TTC	GAC	TGG	GTC	TAC	TAC	528
	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	
					165					170					175		
15	GAG	TCC	CGC	AAC	CAC	GTC	CAC	GTG	TCG	GTC	AAA	GCT	GAT	AAC	TCA	CTG	576
	Glu	Ser	Arg	Asn	His	Val	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	
				180					185					190			
20	GCG	GTC	CGG	GCG	GGC	GGC	TGC	TTT	CCG	GGA	AAT	GCA	ACT	GTG	CGC	CTG	624
	Ala	Val	Arg	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	
			195				200					205					
	TGG	AGC	GGC	GAG	CGG	AAA	GGG	CTG	CGG	GAA	CTG	CAC	CGC	GGA	GAC	TGG	672
	Trp	Ser	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	
		210					215					220					
25	GTT	TTG	GCG	GCC	GAT	GCG	TCA	GGC	CGG	GTG	GTG	CCC	ACG	CCG	GTG	CTG	720
	Val	Leu	Ala	Ala	Asp	Ala	Ser	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	
		225				230					235					240	
30	CTC	TTC	CTG	GAC	CGG	GAC	TTG	CAG	CGC	CGG	GCT	TCA	TTT	GTG	GCT	GTG	768
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	Val	
				245					250						255		
35	GAG	ACC	GAG	TGG	CCT	CCA	CGC	AAA	CTG	TTG	CTC	ACG	CCC	TGG	CAC	CTG	816
	Glu	Thr	Glu	Trp	Pro	Pro	Arg	Lys	Leu	Leu	Leu	Thr	Pro	Trp	His	Leu	
				260					265					270			
40	GTG	TTT	GCC	GCT	CGA	GGG	CCG	GCG	CCC	GCG	CCA	GGC	GAC	TTT	GCA	CCG	864
	Val	Phe	Ala	Ala	Arg	Gly	Pro	Ala	Pro	Ala	Pro	Gly	Asp	Phe	Ala	Pro	
			275				280						285				
	GTG	TTC	GCG	CGC	CGG	CTA	CGC	GCT	GGG	GAC	TCG	GTG	CTG	GCG	CCC	GGC	912
	Val	Phe	Ala	Arg	Arg	Leu	Arg	Ala	Gly	Asp	Ser	Val	Leu	Ala	Pro	Gly	
		290					295					300					
45	GGG	GAT	GCG	CTT	CGG	CCA	GCG	CGC	GTG	GCC	CGT	GTG	GCG	CGG	GAG	GAA	960
	Gly	Asp	Ala	Leu	Arg	Pro	Ala	Arg	Val	Ala	Arg	Val	Ala	Arg	Glu	Glu	
		305				310					315					320	
50	GCC	GTG	GGC	GTG	TTC	GCG	CCG	CTC	ACC	GCG	CAC	GGG	ACG	CTG	CTG	GTG	1008
	Ala	Val	Gly	Val	Phe	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Leu	Leu	Val	
					325					330					335		
55	AAC	GAT	GTC	CTG	GCC	TCT	TGC	TAC	GCG	GTT	CTG	GAG	AGT	CAC	CAG	TGG	1056
	Asn	Asp	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Leu	Glu	Ser	His	Gln	Trp	
				340					345					350			
60	GCG	CAC	CGC	GCT	TTT	GCC	CCC	TTG	AGA	CTG	CTG	CAC	GCG	CTA	GGG	GCG	1104
	Ala	His	Arg	Ala	Phe	Ala	Pro	Leu	Arg	Leu	Leu	His	Ala	Leu	Gly	Ala	
			355					360					365				

CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT	1152
Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser	
370 375 380	

5	CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG	1191
	Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly	
	385 390 395	

10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 1251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1248

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30	ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC	48
	Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile	
	1 5 10 15	

35	AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT	96
	Ser Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
	20 25 30	

40	TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG	144
	Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	

	CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA	192
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys	
	50 55 60	

45	TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT	240
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile	
	65 70 75 80	

50	CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC	288
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn	
	85 90 95	

55	GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG	336
	Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu	
	100 105 110	

60	GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT	384
	Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr	
	115 120 125	

	GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT	432
	Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr	
	130 135 140	
5	GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG	480
	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys	
	145 150 155 160	
10	TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC	528
	Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
	165 170 175	
15	TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT	576
	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
	180 185 190	
20	TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG	624
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val	
	195 200 205	
25	ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC	672
	Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly	
	210 215 220	
30	GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC	720
	Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp	
	225 230 235 240	
35	TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC	768
	Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile	
	245 250 255	
40	GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG	816
	Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala	
	260 265 270	
45	CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA	864
	His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala	
	275 280 285	
50	ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA	912
	Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu	
	290 295 300	
55	GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT	960
	Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr	
	305 310 315 320	
60	GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA	1008
	Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile	
	325 330 335	
65	ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC	1056
	Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His	
	340 345 350	
70	AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG	1104
	Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu	
	355 360 365	

	ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG	1152
	Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu	
	370 375 380	
5	GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG	1200
	Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp	
	385 390 395 400	
10	CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT	1248
	Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser	
	405 410 415	
	TGA	1251

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Val	Glu	Met	Leu	Leu	Leu	Thr	Arg	Ile	Leu	Leu	Val	Gly	Phe	Ile	
1				5					10					15		
Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly	
			20					25					30			
Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
		35					40					45				
Gln	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
	50					55					60					
Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
	65				70					75					80	
Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
			85						90					95		
Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	
			100					105					110			
Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
	115						120					125				
Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
	130					135					140					
Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	
	145				150					155					160	
Tyr	Gly	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	
				165					170					175		

60

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn  
 180 185 190  
 5 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val  
 195 200 205  
 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly  
 210 215 220  
 10 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp  
 225 230 235 240  
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr  
 245 250 255  
 15 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala  
 260 265 270  
 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly  
 275 280 285  
 20 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln  
 290 295 300  
 25 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser  
 305 310 315 320  
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro  
 325 330 335  
 30 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys  
 340 345 350  
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro  
 355 360 365  
 35 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala  
 370 375 380  
 40 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg  
 385 390 395 400  
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His  
 405 410 415  
 45 Pro Leu Gly Met Val Ala Pro Ala Ser  
 420 425

50 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu  
 1 5 10 15  
 5 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
 20 25 30  
 10 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
 35 40 45  
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
 50 55 60  
 15 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn  
 65 70 75 80  
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp  
 85 90 95  
 20 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile  
 100 105 110  
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
 115 120 125  
 25 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly  
 130 135 140  
 30 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly  
 145 150 155 160  
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr  
 165 170 175  
 35 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu  
 180 185 190  
 40 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu  
 195 200 205  
 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp  
 210 215 220  
 45 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu  
 225 230 235 240  
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val  
 245 250 255  
 50 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu  
 260 265 270  
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro  
 275 280 285  
 55 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly  
 290 295 300  
 60 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu



	Met	Ser	Pro	Ala	Trp	Leu	Arg	Pro	Arg	Leu	Arg	Phe	Cys	Leu	Phe	Leu
	1				5					10					15	
35	Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg
				20					25					30		
	Val	Val	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala
			35					40					45			
40	Tyr	Lys	Gln	Phe	Ser	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	Gly	Ala	Ser
		50					55					60				
	Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu
45	65					70					75					80
	Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn
				85						90					95	
50	Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn
				100					105					110		
	Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg
			115					120					125			
55	Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu
		130					135					140				
	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg
60	145					150					155					160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp  
                                   165                                  170                                  175  
 5 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser  
                                   180                                  185                                  190  
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala  
                                   195                                  200                                  205  
 10 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys  
                                   210                                  215                                  220  
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe  
 15 225                                  230                                  235                                  240  
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala  
                                   245                                  250                                  255  
 20 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr  
                                   260                                  265                                  270  
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala  
                                   275                                  280                                  285  
 25 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val  
                                   290                                  295                                  300  
 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val  
 30 305                                  310                                  315                                  320  
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly  
                                   325                                  330                                  335  
 35 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
                                   340                                  345                                  350  
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro  
                                   355                                  360                                  365  
 40 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr  
                                   370                                  375                                  380  
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Ser Thr  
 45 385                                  390                                  395                                  400  
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
                                   405                                  410  
 50

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 437 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5	Met	Leu	Leu	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Val	Ile	Leu	Ala	Ser	Ser	1	5	10	15
	Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	20	25	30	
10	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	35	40	45	
	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	50	55	60	
15	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	65	70	75	80
20	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	85	90	95	
	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	100	105	110	
25	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	115	120	125	
	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	130	135	140	
30	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	145	150	155	160
35	Met	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	165	170	175	
	Glu	Ser	Lys	Ala	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	180	185	190	
40	Ala	Ala	Lys	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	195	200	205	
	Glu	Gln	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	210	215	220	
45	Val	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	225	230	235	240
50	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	245	250	255	
	Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	260	265	270	
55	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	Gly	Pro	Ser	275	280	285	
60	Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	290	295	300	

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser  
305 310 315 320

5 Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala  
325 330 335

His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val  
340 345 350

10 Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu  
355 360 365

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly  
370 375 380

15 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly  
385 390 395 400

20 Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His  
405 410 415

Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met  
420 425 430

25 Ala Val Lys Ser Ser  
435

30 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 418 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser  
1 5 10 15

45 Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg  
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile  
35 40 45

50 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly  
50 55 60

55 Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr  
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg  
85 90 95

60

	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser	100	105	110
5	Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	115	120	125
	Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg	130	135	140
10	Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr	145	150	155
	Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	165	170	175
15	Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	180	185	190
20	Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln	195	200	205
	Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val	210	215	220
25	Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met	225	230	235
	Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu	245	250	255
30	Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu	260	265	270
35	Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala	275	280	285
	Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp	290	295	300
40	Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu	305	310	315
	Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val	325	330	335
45	Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu	340	345	350
50	Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser	355	360	365
	Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn	370	375	380
55	Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	385	390	395
60	Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	405	410	415

Ser Ser

## 5 (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu  
 1 5 10 15  
 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys  
 20 20 25 30  
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile  
 25 35 40 45  
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly  
 50 55 60  
 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr  
 30 65 70 75 80  
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg  
 85 90 95  
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser  
 100 105 110  
 Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp  
 40 115 120 125  
 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg  
 130 135 140  
 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met  
 45 145 150 155 160  
 Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu  
 165 170 175  
 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala  
 50 180 185 190  
 Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu  
 55 195 200 205  
 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val  
 210 215 220  
 Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr  
 60

	225		230		235		240									
	Phe	Leu	Asp	Arg	Asp	Asp	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	Ile	Glu
					245					250					255	
5	Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu
				260					265					270		
	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser
10			275					280					285			
	Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu
		290					295					300				
15	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu
	305					310					315					320
	Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr
					325					330					335	
20	Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly
				340					345					350		
	Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu
25			355					360					365			
	Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His
		370					375					380				
30	Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp
	385					390				395						400
	Ser	Gly	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr
					405					410					415	
35	Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile
				420					425					430		
	His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp
40			435					440					445			
	Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser
		450					455					460				
45	Arg	Gly	Ala	Gly	Gly	Gly	Ala	Arg	Glu	Gly	Ala					
	465					470				475						

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

60	Met	Ser	Pro	Ala	Arg	Leu	Arg	Pro	Arg	Leu	His	Phe	Cys	Leu	Val	Leu
	1					5				10					15	

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg  
 20 25 30  
 5 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala  
 35 40 45  
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser  
 50 55 60  
 10 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu  
 65 70 75 80  
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn  
 85 90 95  
 15 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn  
 100 105 110  
 20 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg  
 115 120 125  
 Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu  
 130 135 140  
 25 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg  
 145 150 155 160  
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp  
 165 170 175  
 30 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser  
 180 185 190  
 35 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala  
 195 200 205  
 Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg  
 210 215 220  
 40 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe  
 225 230 235 240  
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala  
 245 250 255  
 45 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr  
 260 265 270  
 50 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala  
 275 280 285  
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val  
 290 295 300  
 55 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val  
 305 310 315 320  
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly  
 325 330 335  
 60



Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala  
 340 345 350  
 5 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His  
 355 360 365  
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr  
 370 375 380  
 10 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser  
 385 390 395 400  
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser  
 405 410  
 15  
 (2) INFORMATION FOR SEQ ID NO:17:  
 (i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu  
 1 5 10 15  
 30 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg  
 20 25 30  
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe  
 35 35 40 45  
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu  
 50 55 60  
 40 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn  
 65 70 75 80  
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp  
 85 90 95  
 45 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile  
 100 105 110  
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly  
 115 120 125  
 50 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly  
 130 135 140  
 55 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly  
 145 150 155 160  
 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr  
 165 170 175  
 60

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu  
 180 185 190  
 5 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu  
 195 200 205  
 Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp  
 210 215 220  
 10 Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu  
 225 230 235 240  
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val  
 245 250 255  
 15 Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu  
 260 265 270  
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro  
 275 280 285  
 20 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly  
 290 295 300  
 25 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu  
 305 310 315 320  
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val  
 325 330 335  
 30 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp  
 340 345 350  
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala  
 355 360 365  
 35 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser  
 370 375 380  
 40 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly  
 385 390 395

45 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

55 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile  
 1 5 10 15  
 60 Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly  
 20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
 35 40 45  
 5 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys  
 50 55 60  
 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile  
 65 70 75 80  
 10 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn  
 85 90 95  
 Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu  
 100 105 110  
 15 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr  
 115 120 125  
 20 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr  
 130 135 140  
 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys  
 145 150 155 160  
 25 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val  
 165 170 175  
 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn  
 180 185 190  
 30 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val  
 195 200 205  
 35 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly  
 210 215 220  
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp  
 225 230 235 240  
 40 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile  
 245 250 255  
 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala  
 260 265 270  
 45 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala  
 275 280 285  
 50 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu  
 290 295 300  
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr  
 305 310 315 320  
 55 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile  
 325 330 335  
 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His  
 340 345 350  
 60

Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu  
 355 360 365

5 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu  
 370 375 380

Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp  
 385 390 395 400

10 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser  
 405 410 415

15 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1416 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1413

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT AAC CAC AGC TCA GTG CCT TGG GCC AGT GCC GCC AGT GTC ACC 48  
 Met Asp Asn His Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr  
 35 1 5 10 15

TGT CTC TCC CTG GGA TGC CAA ATG CCA CAG TTC CAG TTC CAG TTC CAG 96  
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln  
 20 25 30

40 CTC CAA ATC CGC AGC GAG CTC CAT CTC CGC AAG CCC GCA AGA AGA ACG 144  
 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr  
 35 40 45

45 CAA ACG ATG CGC CAC ATT GCG CAT ACG CAG CGT TGC CTC AGC AGG CTG 192  
 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu  
 50 55 60

ACC TCT CTG GTG GCC CTG CTG CTG ATC GTC TTG CCG ATG GTC TTT AGC 240  
 Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser  
 65 70 75 80

CCG GCT CAC AGC TGC GGT CCT GGC CGA GGA TTG GGT CGT CAT AGG GCG 288  
 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala  
 85 90 95

55 CGC AAC CTG TAT CCG CTG GTC CTC AAG CAG ACA ATT CCC AAT CTA TCC 336  
 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser  
 100 105 110

60

	GAG TAC ACG AAC AGC GCC TCC GGA CCT CTG GAG GGT GTG ATC CGT CGG	384
	Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	
	115 120 125	
5	GAT TCG CCC AAA TTC AAG GAC CTC GTG CCC AAC TAC AAC AGG GAC ATC	432
	Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	
	130 135 140	
10	CTT TTC CGT GAC GAG GAA GGC ACC GGA GCG GAT GGC TTG ATG AGC AAG	480
	Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	
	145 150 155 160	
15	CGC TGC AAG GAG AAG CTA AAC GTG CTG GCC TAC TCG GTG ATG AAC GAA	528
	Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	
	165 170 175	
20	TGG CCC GGC ATC CGG CTG CTG GTC ACC GAG AGC TGG GAC GAG GAC TAC	576
	Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	
	180 185 190	
25	CAT CAC GGC CAG GAG TCG CTC CAC TAC GAG GGC CGA GCG GTG ACC ATT	624
	His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	
	195 200 205	
30	GCC ACC TCC GAT CGC GAC CAG TCC AAA TAC GGC ATG CTC GCT CGC CTG	672
	Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	
	210 215 220	
35	GCC GTC GAG GCT GGA TTC GAT TGG GTC TCC TAC GTC AGC AGG CGC CAC	720
	Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	
	225 230 235 240	
40	ATC TAC TGC TCC GTC AAG TCA GAT TCG TCG ATC AGT TCC CAC GTG CAC	768
	Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	
	245 250 255	
45	GGC TGC TTC ACG CCG GAG AGC ACA GCG CTG CTG GAG AGT GGA GTC CGG	816
	Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg	
	260 265 270	
50	AAG CCG CTC GGC GAG CTC TCT ATC GGA GAT CGT GTT TTG AGC ATG ACC	864
	Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr	
	275 280 285	
55	GCC AAC GGA CAG GCC GTC TAC AGC GAA GTG ATC CTC TTC ATG GAC CGC	912
	Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg	
	290 295 300	
60	AAC CTC GAG CAG ATG CAA AAC TTT GTG CAG CTG CAC ACG GAC GGT GGA	960
	Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly	
	305 310 315 320	
65	GCA GTG CTC ACG GTG ACG CCG GCT CAC CTG GTT AGC GTT TGG CAG CCG	1008
	Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro	
	325 330 335	
70	GAG AGC CAG AAG CTC ACG TTT GTG TTT GCG CAT CGC ATC GAG GAG AAG	1056
	Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys	
	340 345 350	

	AAC CAG GTG CTC GTA CGG GAT GTG GAG ACG GGC GAG CTG AGG CCC CAG	1104
	Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln	
	355 360 365	
5	CGA GTG GTC AAG TTG GGC AGT GTG CGC AGT AAG GGC GTG GTC GCG CCG	1152
	Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro	
	370 375 380	
10	CTG ACC CGC GAG GGC ACC ATT GTG GTC AAC TCG GTG GCC GCC AGT TGC	1200
	Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys	
	385 390 395 400	
15	TAT GCG GTG ATC AAC AGT CAG TCG CTG GCC CAC TGG GGA CTG GCT CCC	1248
	Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro	
	405 410 415	
20	ATG CGC CTG CTG TCC ACG CTG GAG GCG TGG CTG CCC GCC AAG GAG CAG	1296
	Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln	
	420 425 430	
25	TTG CAC AGT TCG CCG AAG GTG GTG AGC TCG GCG CAG CAG CAG AAT GGC	1344
	Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly	
	435 440 445	
30	ATC CAT TGG TAT GCC AAT GCG CTC TAC AAG GTC AAG GAC TAC GTG CTG	1392
	Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu	
	450 455 460	
35	CCG CAG AGC TGG CGC CAC GAT TGA	1416
	Pro Gln Ser Trp Arg His Asp	
	465 470	
40	(2) INFORMATION FOR SEQ ID NO:20:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 471 amino acids	
	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
50	Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr	
	1 5 10 15	
55	Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln	
	20 25 30	
60	Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	
	35 40 45	
65	Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	
	50 55 60	
70	Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser	
	65 70 75 80	
75	Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	

	85	90	95
	Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser		
	100	105	110
5	Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg		
	115	120	125
	Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile		
10	130	135	140
	Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys		
	145	150	155
15	Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu		
	165	170	175
	Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr		
	180	185	190
20	His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile		
	195	200	205
	Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu		
25	210	215	220
	Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His		
	225	230	235
30	Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His		
	245	250	255
	Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg		
	260	265	270
35	Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr		
	275	280	285
	Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg		
40	290	295	300
	Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly		
	305	310	315
45	Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro		
	325	330	335
	Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys		
	340	345	350
50	Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln		
	355	360	365
	Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro		
55	370	375	380
	Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys		
	385	390	395
60	Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro		

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5      405      410      415
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
      420      425      430

10    Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
      435      440      445

15    Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
      450      455      460

      Pro Gln Ser Trp Arg His Asp
      465      470

20    (2) INFORMATION FOR SEQ ID NO:21:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 221 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: peptide

      (v) FRAGMENT TYPE: internal

25

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

30    Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
      1          5          10          15

      Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
      20          25          30

35    Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
      35          40          45

      Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
      50          55          60

      Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
      65          70          75          80

45    Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
      85          90          95

      Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
      100          105          110

50    Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
      115          120          125

      Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
      130          135          140

      Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
      145          150          155          160

60    Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe

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	165	170	175
	Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val		
	180	185	190
5	Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly		
	195	200	205
10	Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg		
	210	215	220

## (2) INFORMATION FOR SEQ ID NO:22:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide  
 (v) FRAGMENT TYPE: internal

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys	
	1	15
30	Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu	
	20	30
35	Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa	
	35	45
	Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile	
	50	60
40	Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg	
	65	80
	Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp	
	85	95
45	Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His	
	100	110
50	His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr	
	115	125
	Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala	
	130	140
55	Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa	
	145	160
60	His Xaa Ser Val Lys Xaa Xaa	
	165	